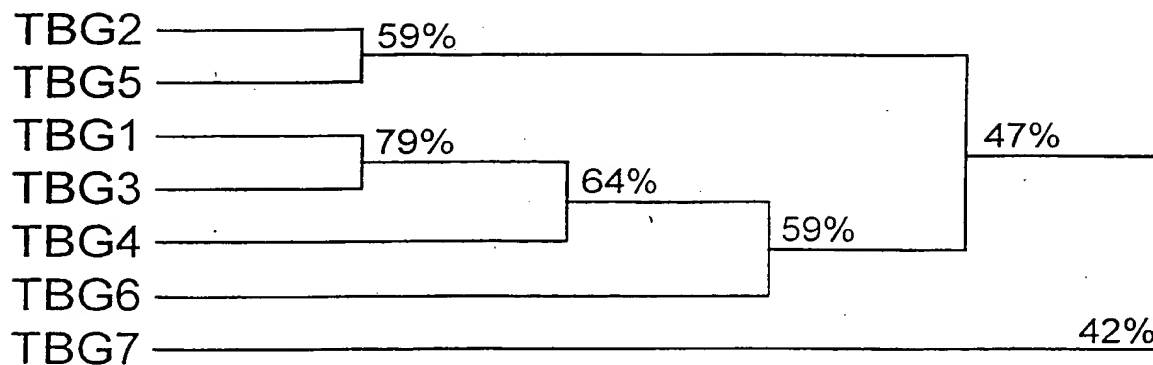
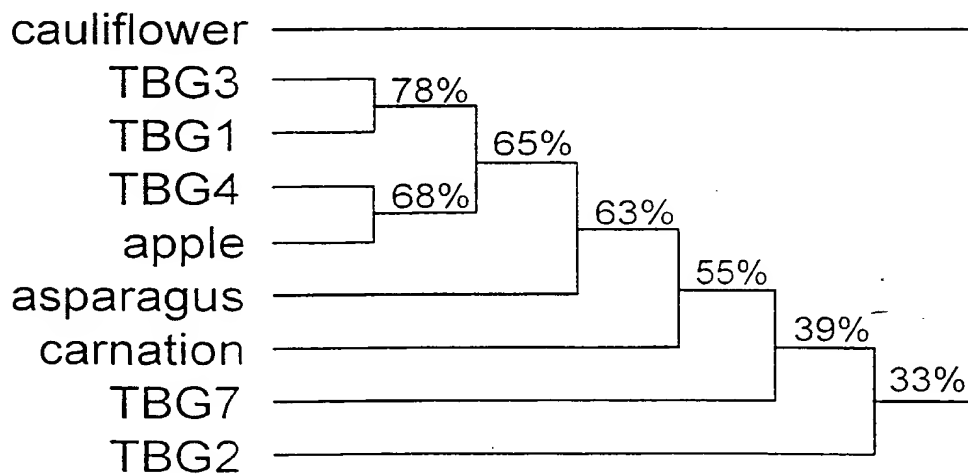


A



B



**Figure 1.  $\beta$ -Galactosidase phylogenetic tree based on shared amino acid sequence identity. A. Tomato  $\beta$ -galactosidase (TBG) cDNAs. B. Plant  $\beta$ -galactosidases. Higgins-Sharp algorithm (UPGMA method)**

Figure 2  
Sheet 1 of 12

Gene/clone name: TBG1/pZBQ2-1-10; accession number AF023847; sequence ID number 1

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TTTTCCTTTGTTCTTTTGCTCAGCACTAG 30
31 AGCCTAGAAGAAGGAAAAAAGAAGTATGGACTAATGGAATAAACATAAAAAAGAGAGAAAAAAGAAGAAATCTTCAGACAACA 122
123 AAAACAGCTGTTTCCCTTCACTACTTTTTCCTCCCAATCTCTATATAATTGCAAGAATAGATAAAGTTGCAACTTGATTAAAAAACA 214
215 GAATAATAAGCTGTGGGGTAGGGAGGAAGTTAGTTTCATTAGTTTCATTGCTTGTAAAGGCACAATCTTGATTCTTGATTGTTGACAAAT 305

306 ATG GGT TTT TGG ATG GCA ATG TTG CTG ATG TTG TTA TTG TGT TTA TGG GTT TCT TGT GGA ATT GCT TCT 374
1 Met Gly Phe Trp Met Ala Met Leu Leu Met Leu Leu Cys Leu Trp Val Ser Cys Gly Ile Ala Ser 23

375 GTT TCA TAT GAC CAT AAA GCT ATC ATT GTA AAT GGA CAA AGA AAA ATT CTC ATT TCT GGA TCC ATT CAC 443
24 Val Ser Tyr Asp His Lys Ala Ile Ile Val Asn Gly Gln Arg Lys Ile Leu Ile Ser Gly Ser Ile His 46

444 TAC CCT AGA AGC ACC CCT GAG ATG TGG CCA GAT CTT ATT CAG AAG GCA AAA GAA GGG GGA GTT GAT GTT 512
47 Tyr Pro Arg Ser Thr Pro Glu Met Trp Pro Asp Leu Ile Gln Lys Ala Lys Glu Gly Val Asp Val 69

513 ATA CAG ACT TAT GTT TTC TGG AAT GGG CAT GAG CCT GAA GAA GGG AAA TAT TAT TTT GAA GAG AGG TAT 581
70 Ile Gln Thr Tyr Val Phe Trp Asn Gly His Glu Pro Glu Glu Gly Lys Tyr Tyr Phe Glu Glu Arg Tyr 92

582 GAT TTA GTG AAG TTC ATT AAA GTG GTG CAA GAA GCA GGA CTT TAT GTG CAT CTT AGG ATT GGA CCT TAT 650
93 Asp Leu Val Lys Phe Ile Lys Val Val Gln Glu Ala Gly Leu Tyr Val His Leu Arg Ile Gly Pro Tyr 115

651 GCA TGT GCT GAA TGG AAT TTT GGG GGT TTT CCT GTT TGG CTG AAG TAT GTT CCA GGT ATT AGT TTC AGA 719
116 Ala Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro Gly Ile Ser Phe Arg 138

720 ACA AAC AAT GAG CCA TTC AAG GCT GCA ATG CAA AAG TTC ACT ACT AAG ATT GTT GAT ATG ATG AAA GCA 788
139 Thr Asn Asn Glu Pro Phe Lys Ala Ala Met Gln Lys Phe Thr Thr Lys Ile Val Asp Met Met Lys Ala 161

789 GAA AAG CTC TAT GAA ACT CAG GGT GGT CCA ATT ATT CTA TCT CAG ATA GAA AAT GAA TAT GGA CCT ATG 857
162 Glu Lys Leu Tyr Glu Thr Gln Gly Gly Pro Ile Ile Leu Ser Gln Ile Glu Asn Glu Tyr Gly Pro Met 184

858 GAG TGG GAA CTA GGT GAA CCT GGT AAA GTT TAC TCA GAA TGG GCA GCC AAA ATG GCT GTG GAT CTT GGC 926
185 Glu Trp Glu Leu Gly Glu Pro Gly Lys Val Tyr Ser Glu Trp Ala Ala Lys Met Ala Val Asp Leu Gly 207

927 ACT GGT GTC CCA TGG ATC ATG TGC AAG CAA GAT GAT GTC CCT GAT CCT ATT ATT AAT ACT TGC AAT GGT 995
208 Thr Gly Val Pro Trp Ile Met Cys Lys Gln Asp Asp Val Pro Asp Pro Ile Ile Asn Thr Cys Asn Gly 230

996 TTC TAC TGT GAC TAC TTC ACA CCA AAT AAG GCT AAT AAA CCC AAG ATG TGG ACT GAA GCC TGG ACA GCC 1064
231 Phe Tyr Cys Asp Tyr Phe Thr Pro Asn Lys Ala Asn Lys Pro Lys Met Trp Thr Glu Ala Trp Thr Ala 253

1065 TGG TTT ACC GAA TTT GGA GGT CCA GTT CCT TAC CGT CCT GCA GAG GAT ATG GCA TTT GCT GTC GCA AGA 1133
254 Trp Phe Thr Glu Phe Gly Gly Pro Val Pro Tyr Arg Pro Ala Glu Asp Met Ala Phe Ala Val Ala Arg 276

1134 TTT ATA CAA ACG GGA GGC TCC TTC ATC AAT TAC TAT ATG TAT CAT GGA GGA ACA AAC TTT GGA AGG ACT 1202
277 Phe Ile Gln Thr Gly Gly Ser Phe Ile Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly Arg Thr 299

1203 TCT GGT GGC CCA TTT ATT GCT ACT AGT TAT GAT TAT GAT GCA CCC CTA GAT GAA TTT GGG TCA TTA CGG 1271
300 Ser Gly Gly Pro Phe Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Phe Gly Ser Leu Arg 322

1272 CAG CCT AAA TGG GGT CAT CTG AAA GAT CTA CAT AGA GCA ATA AAG CTC TGT GAG CCA GCT TTA GTA TCT 1340
323 Gln Pro Lys Trp Gly His Leu Lys Asp Leu His Arg Ala Ile Lys Leu Cys Glu Pro Ala Leu Val Ser 345

1341 GTA GAT CCA ACT GTG ACA TCC TTA GGA AAC TAT CAA GAG GCA CGT GTT TTC AAG TCA GAG TCT GGG GCC 1409
346 Val Asp Pro Thr Val Thr Ser Leu Gly Asn Tyr Gln Glu Ala Arg Val Phe Lys Ser Glu Ser Gly Ala 368

1410 TGC GCT GCC TTC CTA GCA AAT TAC AAC CAG CAC TCT TTT GCT AAA GTG GCA TTT GGG AAC ATG CAT TAT 1478
369 Cys Ala Ala Phe Leu Ala Asn Tyr Asn Gln His Ser Phe Ala Lys Val Ala Phe Gly Asn Met His Tyr 391

1479 AAC TTG CCA CCC TGG TCT ATC AGC ATT CTT CCC GAC TGC AAG AAC ACT GTC TAT AAT ACT GCA AGG GTT 1547
392 Asn Leu Pro Pro Trp Ser Ile Ser Ile Leu Pro Asp Cys Lys Asn Thr Val Tyr Asn Thr Ala Arg Val 414

1548 GGT GCT CAA AGT GCT CAG ATG AAG ATG ACT CCA GTC AGT AGA GGA TTC TCA TGG GAG TCA TTC AAT GAA 1616
415 Gly Ala Gln Ser Ala Gln Met Lys Met Thr Pro Val Ser Arg Gly Phe Ser Trp Glu Ser Phe Asn Glu 437

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Figure 2  
Sheet 2 of 12

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Gene/clone name: TBG1/pZBG2-10; accession number AF023847; Sequence ID number 1 cont.

1617	GAC	GCA	GCA	TCG	CAT	GAA	GAC	GAC	ACT	TTC	ACA	GTT	GTT	GGG	TTA	TTC	GAG	CAG	ATT	AAT	ATC	ACA	AGA	1685
438	Asp	Ala	Ala	Ser	His	Glu	Asp	Asp	Thr	Phe	Thr	Val	Val	Gly	Leu	Leu	Glu	Gln	Ile	Asn	Ile	Thr	Arg	460
1686	GAT	GTA	TCT	GAT	TAC	TTG	TGG	TAT	ATG	ACT	GAC	ATT	GAG	ATT	GAT	CCA	ACA	GAA	GGA	TTT	TTG	AAT	AGT	1754
461	Asp	Val	Ser	Asp	Tyr	Leu	Trp	Tyr	Met	Thr	Asp	Ile	Glu	Ile	Asp	Pro	Thr	Glu	Gly	Phe	Leu	Asn	Ser	483
1755	GGA	AAT	TGG	CCT	TGG	CTT	ACT	GTC	TTT	TCT	GCT	GGC	CAT	GCA	TTG	CAT	GTA	TTC	GTG	AAT	GGT	CAA	TTA	1823
484	Gly	Asn	Trp	Pro	Trp	Leu	Thr	Val	Phe	Ser	Ala	Gly	His	Ala	Leu	His	Val	Phe	Val	Asn	Gly	Gln	Leu	506
1824	GCA	GGA	ACT	GTG	TAC	GGA	AGT	TTA	GAA	AAC	CCA	AAA	CTA	ACT	TTC	AGC	AAC	GGT	ATA	AAT	CTG	AGA	GCT	1892
507	Ala	Gly	Thr	Val	Tyr	Gly	Ser	Leu	Glu	Asn	Pro	Lys	Leu	Thr	Phe	Ser	Asn	Gly	Ile	Asn	Leu	Arg	Ala	529
1893	GGT	GTG	AAC	AAG	ATT	TCT	CTG	CTA	AGC	ATT	GCT	GTT	GGT	CTT	CCG	AAC	GTT	GGC	CCT	CAT	TTT	GAG	ACA	1961
530	Gly	Val	Asn	Lys	Ile	Ser	Leu	Leu	Ser	Ile	Ala	Val	Gly	Leu	Pro	Asn	Val	Gly	Pro	His	Phe	Glu	Thr	552
1962	TGG	AAT	GCT	GGT	GTT	CTT	GGA	CCA	GTT	TCA	CTT	AAT	GGA	CTT	AAT	GAA	GGA	ACA	AGA	GAT	TTA	ACA	TGG	2030
553	Trp	Asn	Ala	Gly	Val	Leu	Gly	Pro	Val	Ser	Leu	Asn	Gly	Leu	Asn	Glu	Gly	Thr	Arg	Asp	Leu	Thr	Trp	575
2031	CAG	AAA	TGG	TTC	TAC	AAG	GTT	GGT	CTA	AAA	GGA	GAA	GCC	CTG	AGT	CTT	CAT	TCA	CTC	AGT	GGT	AGC	CCA	2099
576	Gln	Lys	Trp	Phe	Tyr	Lys	Val	Gly	Leu	Lys	Gly	Glu	Ala	Leu	Ser	Leu	His	Ser	Leu	Ser	Gly	Ser	Pro	598
2100	TCC	GTG	GAG	TGG	GTG	GAA	GGC	TCT	TTA	GTG	GCT	CAG	AAG	CAG	CCA	CTC	AGT	TGG	TAT	AAG	ACT	ACA	TTC	2168
599	Ser	Val	Glu	Trp	Val	Glu	Gly	Ser	Leu	Val	Ala	Gln	Lys	Gln	Pro	Leu	Ser	Trp	Tyr	Lys	Thr	Thr	Phe	621
2169	AAT	GCT	CCA	GAT	GGA	AAT	GAA	CCT	TTG	GCT	TTA	GAT	ATG	AAT	ACC	ATG	GGC	AGT	GCT	CAA	GTA	TGG	ATA	2237
622	Asn	Ala	Pro	Asp	Gly	Asn	Glu	Pro	Leu	Ala	Leu	Asp	Met	Asn	Thr	Met	Gly	Lys	Gly	Gln	Val	Trp	Ile	644
2238	AAT	GGT	CAG	AGC	CTC	GGA	CGC	CAC	TGG	CCT	GCA	TAT	AAA	TCA	TCT	GGA	AGT	TGT	AGT	GTC	TGT	AAC	TAT	2306
645	Asn	Gly	Gln	Ser	Leu	Gly	Arg	His	Trp	Pro	Ala	Tyr	Lys	Ser	Ser	Gly	Ser	Cys	Ser	Val	Cys	Asn	Tyr	667
2307	ACT	GGC	TGG	TTT	GAT	GAG	AAA	AAG	TGC	CTA	ACT	AAC	TGT	GGT	GAG	GGC	TCA	CAA	AGA	TGG	TAC	CAC	GTA	2375
668	Thr	Gly	Trp	Phe	Asp	Glu	Lys	Lys	Cys	Leu	Thr	Asn	Cys	Gly	Glu	Gly	Ser	Gln	Arg	Trp	Tyr	His	Val	690
2376	CCC	CGG	TCT	TGG	CTG	TAT	CCT	ACT	GGA	AAT	TTG	TTA	GTT	GTA	TTC	GAG	GAA	TGG	GGA	GGA	GAT	CCT	TAT	2444
691	Pro	Arg	Ser	Trp	Leu	Tyr	Pro	Thr	Gly	Asn	Leu	Leu	Val	Val	Phe	Glu	Glu	Trp	Gly	Gly	Asp	Pro	Tyr	713
2445	GGA	ATC	ACT	TTA	GTC	AAA	AGA	GAA																

### Figure 2

She t 3 of 12

Gene/clone name: TBG2/pZBG2-1-12; accession number AF154420; Sequence ID number 2

1																					GG	2		
3	AGC	AGA	AGA	AAA	ACA	CTG	AAT	TTT	CCG	TTA	ATA	CTA	ACG	GTG	TTA	ACT	ATC	CAC	TTT	GTG	ATC	GTC	GCC	71
1	Ser	Arg	Arg	Lys	Thr	Leu	Asn	Phe	Pro	Leu	Ile	Leu	Thr	Val	Leu	Thr	Ile	His	Phe	Val	Ile	Val	Ala	23
72	GGC	GAG	TAT	TTC	AAG	CCG	TTC	AAT	GTC	ACC	TAC	GAT	AAC	CGA	GCT	CTC	ATC	ATC	GGC	GGT	AAA	CGC	CGT	140
24	Gly	Glu	Tyr	Phe	Lys	Pro	Phe	Asn	Val	Thr	Tyr	Asp	Asn	Arg	Ala	Leu	Ile	Ile	Gly	Gly	Lys	Arg	Arg	46
141	ATG	CTT	ATC	TCC	GCC	GGA	ATT	CAC	TAC	CCT	CGC	GCC	ACT	CCT	GAG	ATG	TGG	CCC	ACA	TTG	ATA	GCT	AGG	209
47	Met	Leu	Ile	Ser	Ala	Gly	Ile	His	Tyr	Pro	Arg	Ala	Thr	Pro	Glu	Met	Trp	Pro	Thr	Leu	Ile	Ala	Arg	69
210	AGC	AAA	GAA	GGT	GGT	GCA	GAT	GTC	ATC	GAG	ACT	TAT	ACA	TTT	TGG	AAT	GGT	CAT	GAG	CCA	ACC	AGG	GGA	278
70	Ser	Lys	Glu	Gly	Gly	Ala	Asp	Val	Ile	Glu	Thr	Tyr	Thr	Phe	Trp	Asn	Gly	His	Glu	Pro	Thr	Arg	Gly	92
279	CAG	TAC	AAT	TTT	GAA	GGA	AGA	TAT	GAT	ATT	GTC	AAG	TTC	GCA	AAG	CTA	GTC	GGA	TCT	CAT	GGA	CTG	TTC	347
93	Gln	Tyr	Asn	Phe	Glu	Gly	Arg	Tyr	Asp	Ile	Val	Lys	Phe	Ala	Lys	Leu	Val	Gly	Ser	His	Gly	Leu	Phe	115
348	CTC	TTT	ATT	CGA	ATA	GGT	CCT	TAT	GCC	TGT	GCA	GAA	TGG	AAC	TTC	GGG	GGA	TTC	CCC	ATA	TGG	CTT	CGT	416
116	Leu	Phe	Ile	Arg	Ile	Gly	Pro	Tyr	Ala	Cys	Ala	Glu	Trp	Asn	Phe	Gly	Gly	Phe	Pro	Ile	Trp	Leu	Arg	138
417	GAT	ATA	CCT	GGA	ATA	GAA	TTT	CGA	ACA	GAT	AAT	GCA	CCA	TTC	AAG	GAG	GAG	ATG	GAG	CGC	TAT	GTT	AAA	485
139	Asp	Ile	Pro	Gly	Ile	Glu	Phe	Arg	Thr	Asp	Asn	Ala	Pro	Phe	Lys	Glu	Glu	Met	Glu	Arg	Tyr	Val	Lys	161
486	AAG	ATA	GTT	GAT	CTT	ATG	ATA	TCT	GAG	TCG	CTC	TTT	TCG	TGG	CAA	GGT	GGT	CCT	ATC	ATT	TTG	CTG	CAG	554
162	Lys	Ile	Val	Asp	Leu	Met	Ile	Ser	Glu	Ser	Leu	Phe	Ser	Trp	Gln	Gly	Gly	Pro	Ile	Ile	Leu	Leu	Gln	184
555	ATT	GAA	AAT	GAA	TAT	GGA	AAT	GTT	GAA	AGC	TCA	TTC	GGT	CCC	AAG	GGG	AAG	TTA	TAT	ATG	AAA	TGG	GCT	623
185	Ile	Glu	Asn	Glu	Tyr	Gly	Asn	Val	Glu	Ser	Ser	Phe	Gly	Pro	Lys	Gly	Lys	Leu	Tyr	Met	Lys	Trp	Ala	207
624	GCT	GAA	ATG	GCT	GTT	GGT	CTT	GGT	GCT	GGT	GTT	CCA	TGG	GTC	ATG	TGC	AGG	CAA	ACT	GAT	GCT	CCA	GAA	692
208	Ala	Glu	Met	Ala	Val	Gly	Leu	Gly	Ala	Gly	Val	Pro	Trp	Val	Met	Cys	Arg	Gln	Thr	Asp	Ala	Pro	Glu	230
693	TAC	ATC	ATA	GAT	ACT	TGT	AAT	GCA	TAC	TAT	TGT	GAT	GGG	TTC	ACG	CCG	AAT	TCC	GAG	AAG	AAA	CCG	AAA	761
231	Tyr	Ile	Ile	Asp	Thr	Cys	Asn	Ala	Tyr	Tyr	Cys	Asp	Gly	Phe	Thr	Pro	Asn	Ser	Glu	Lys	Lys	Pro	Lys	253
762	ATT	TGG	ACT	GAG	AAT	TGG	AAT	GGA	TGG	TTT	GCA	GAT	TGG	GGT	GAA	AGA	CTT	CCA	TAT	AGA	CCT	TCC	GAG	830
254	Ile	Trp	Thr	Glu	Asn	Trp	Asn	Gly	Trp	Phe	Ala	Asp	Trp	Gly	Glu	Arg	Leu	Pro	Tyr	Arg	Pro			

Figur 2

Sheet 4 of 12

Gene/clone name: TBG2/pZBG2-2; accession number AF154420; Sequence ID number 2 cont.

1383	CTA AAA GCA AGC TCG GAA AGT TTT TCA CAA TCT TGG ATG ACA TTG AAG GAG CCA CTT GGT GTG TGG GGT	1451
461	Leu Lys Ala Ser Ser Glu Ser Phe Ser Gln Ser Trp Met Thr Leu Lys Glu Pro Leu Gly Val Trp Gly	483
1452	GAC AAG AAT TTC ACT TCT AAA GGA ATA CTG GAG CAT CTG AAT GTG ACA AAA GAC CAG TCT GAT TAC CTG	1520
484	Asp Lys Asn Phe Thr Ser Lys Gly Ile Leu Glu His Leu Asn Val Thr Lys Asp Gln Ser Asp Tyr Leu	506
1521	TGG TAT CTG ACC AGG ATA TAT ATT TCT GAT GAT GAC ATC TCA TTT TGG GAG GAA AAT GAT GTT AGT CCA	1589
507	Trp Tyr Leu Thr Arg Ile Tyr Ile Ser Asp Asp Asp Ile Ser Phe Trp Glu Glu Asn Asp Val Ser Pro	529
1590	ACA ATT GAT ATT GAT AGC ATG CGT GAT TTT GTT CGC ATT TTT GTT AAT GGG CAG CTT GCA GGT AGT GTG	1658
530	Thr Ile Asp Ile Asp Ser Met Arg Asp Phe Val Arg Ile Phe Val Asn Gly Gln Leu Ala Gly Ser Val	552
1659	AAA GGC AAA TGG ATC AAG GTG GTT CAA CCT GTT AAG CTG GTT CAG GGA TAC AAC GAC ATA CTG CTA TTA	1727
553	Lys Gly Lys Trp Ile Lys Val Val Gln Pro Val Lys Leu Val Gln Gly Tyr Asn Asp Ile Leu Leu Leu	575
1728	TCT GAG ACG GTG GGA TTG CAG AAT TAT GGT GCC TTC TTG GAG AAG GAT GGG GCA GGT TTT AAA GGT CAG	1796
576	Ser Glu Thr Val Gly Leu Gln Asn Tyr Gly Ala Phe Leu Glu Lys Asp Gly Ala Gly Phe Lys Gly Gln	598
1797	ATA AAG CTT ACA GGA TGC AAA AGC GGG GAT ATC AAT CTC ACA ACA TCT TTA TGG ACC TAC CAG GTG GGG	1865
599	Ile Lys Leu Thr Gly Cys Lys Ser Gly Asp Ile Asn Leu Thr Thr Ser Leu Trp Thr Tyr Gln Val Gly	621
1866	CTT AGA GGC GAA TTC CTG GAA GTA TAT GAT GTC AAT AGT ACT GAA AGT GCA GGA TGG ACT GAG TTT CCC	1934
622	Leu Arg Gly Glu Phe Leu Glu Val Tyr Asp Val Asn Ser Thr Glu Ser Ala Gly Trp Thr Glu Phe Pro	644
1935	ACT GGT ACA ACT CCG TCA GTC TTT TCG TGG TAC AAG ACA AAG TTT GAT GCC CCA GGC GGG ACA GAT CCA	2003
645	Thr Gly Thr Thr Pro Ser Val Phe Ser Trp Tyr Lys Thr Lys Phe Asp Ala Pro Gly Gly Thr Asp Pro	667
2004	GTT GCT CTT GAT TTT AGT AGC ATG GGA AAA GGT CAG GCA TGG GTT AAT GGC CAC CAT GTA GGA AGA TAT	2072
668	Val Ala Leu Asp Phe Ser Ser Met Gly Lys Gly Gln Ala Trp Val Asn Gly His His Val Gly Arg Tyr	690
2073	TGG ACT TTG GTT GCA CCA AAT AAT GGA TGT GGA AGA ACT TGT GAT TAT CGT GGT GCT TAC CAC TCT GAT	2141
691	Trp Thr Leu Val Ala Pro Asn Asn Gly Cys Gly Arg Thr Cys Asp Tyr Arg Gly Ala Tyr His Ser Asp	713
2142	AAA TGT AGG ACA AAC TGT GGA GAG ATT ACT CAG GCC TGG TAC CAT ATA CCT AGA TCA TGG CTA AAG ACA	2210
714	Lys Cys Arg Thr Asn Cys Gly Glu Ile Thr Gln Ala Trp Tyr His Ile Pro Arg Ser Trp Leu Lys Thr	736
2211	TTA AAT AAT GTA CTA GTT ATC TTT GAA GAA ACA GAT AAA ACT CCG TTT GAT ATT TCC ATT TCT ACG CGT	2279
737	Leu Asn Asn Val Leu Val Ile Phe Glu Glu Thr Asp Lys Thr Pro Phe Asp Ile Ser Ile Ser Thr Arg	759
2280	TCT ACT GAA ACC ATT TGT GCT CAA GTA TCG GAA AAG CAC TAT CCA CCT CTA CAT AAG TGG TCT CAT TCG	2348
760	Ser Thr Glu Thr Ile Cys Ala Gln Val Ser Glu Lys His Tyr Pro Pro Leu His Lys Trp Ser His Ser	782
2349	GAG TTT GAC AGA AAG TTG TCT CTG ATG GAT AAA ACA CCA GAA ATG CAC TTG CAG TGT GAC GAA GGA CAT	2417
783	Glu Phe Asp Arg Lys Leu Ser Leu Met Asp Lys Thr Pro Glu Met His Leu Gln Cys Asp Glu Gly His	805
2418	ACA ATC TCT TCT ATT GAA TTT GCA AGC TAT GGA AGT CCG AAT GGC AGC TGT CAA AAG TTC TCA CAA GGA	2486
806	Thr Ile Ser Ser Ile Glu Phe Ala Ser Tyr Gly Ser Pro Asn Gly Ser Cys Gln Lys Phe Ser Gln Gly	828
2487	AAA TGC CAT GCT GCA AAT TCC TTG TCT GTT GTA TCT CAG GCT TGT ATA GGA AGA ACT AGT TGC AGC ATT	2555
829	Lys Cys His Ala Ala Asn Ser Leu Ser Val Val Ser Gln Ala Cys Ile Gly Arg Thr Ser Cys Ser Ile	851
2556	GGC ATT TCC AAT GGT GTA TTT GGA GAT CCA TGT CGA CAC GTT GTG AAG AGT TTG GCT GTT CAA GCA AAA	2624
852	Gly Ile Ser Asn Gly Val Phe Gly Asp Pro Cys Arg His Val Val Lys Ser Leu Ala Val Gln Ala Lys	874
2625	TGC TCA CCA CCA CCA GAC CTC AGC ACT TCA GCT TCC TCG TGA GGAGACTCTGGTAACACGTTAACCTTTTAGAACGAA	2702
875	Cys Ser Pro Pro Pro Asp Leu Ser Thr Ser Ala Ser Ser ...	888
2703	ACGATCCCTTAAAGTCCACTCGTTCCCTCGCCCCGAGCCCTCTGCTACATTTCTCAGATCGCATCGTTACAATCAGGCGGAGAAAAACGTAC	2794
2795	ATGGACGATTTTACTTGTAATATTTGGTTACTGTATATAAATGAAAGGAATAATGTTGCTTATGCATATGAGCTGCAAAATTATATGACAA	2886
2887	AGTAACAAATGAAAATAGAAAACCTCTGTCTGTCAAAGAATTTTAAACAACACCATTTATTAAAGTTAGTTAACATGATTAATAAAAAA	2978
2979	AAAAAA	2984

Figure 2

She 15 of 12

Gene/clone name: TBG3/p2- Oc/bl; accession number AF154421; Sequence ID number 3

1 AGAGTTCATTATTTTTTTTTCATTTTGAA 30  
31 AAGAGGAAAAAATAAGTTAAAGGGGGGAAAAAGTTTTCATTTTGCTTAAAAAGGCACAATCTTGATAGAAAAGGAGATAATTTTAC 121

122 ATG GGT TGT ACG CTT ATA CTA ATG TTG AAT GTG TTG TTG GTG TTG TTG GGT TCA TGG GTT TTT TCT GGA 190  
1 Met Gly Cys Thr Leu Ile Leu Met Leu Asn Val Leu Leu Val Leu Leu Gly Ser Trp Val Phe Ser Gly 23

191 ACA GCT TCT GTT TCA TAT GAC CAT AGG GCT ATT ATT GTA AAT GGA CAA AGA AGA ATA CTT ATT TCT GGT 259  
24 Thr Ala Ser Val Ser Tyr Asp His Arg Ala Ile Ile Val Asn Gly Gln Arg Arg Ile Leu Ile Ser Gly 46

260 TCT GTT CAT TAT CCA AGA AGC ACT CCT GAG ATG TGG CCA GGT ATT ATT CAA AAG GCT AAA GAA GGA GGT 328  
47 Ser Val His Tyr Pro Arg Ser Thr Pro Glu Met Trp Pro Gly Ile Ile Gln Lys Ala Lys Glu Gly Gly 69

329 GTG GAT GTG ATT CAG ACT TAT GTT TTC TGG AAT GGA CAT GAG CCT CAA CAA GGG AAA TAT TAT TTT GAA 397  
70 Val Asp Val Ile Gln Thr Tyr Val Phe Trp Asn Gly His Glu Pro Gln Gln Gly Lys Tyr Tyr Phe Glu 92

398 GGG AGA TAT GAT TTA GTG AAG TTT ATT AAG CTG GTG CAC CAA GCA GGA CTT TAT GTC CAT CTT AGA GTT 466  
93 Gly Arg Tyr Asp Leu Val Lys Phe Ile Lys Leu Val His Gln Ala Gly Leu Tyr Val His Leu Arg Val 115

467 GGA CCT TAT GCT TGT GCT GAA TGG AAT TTT GGG GGC TTT CCT GTT TGG CTG AAA TAT GTT CCA GGT ATC 535  
116 Gly Pro Tyr Ala Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro Gly Ile 138

536 AGT TTC AGA ACA GAT AAT GGA CCT TTC AAG GCT GCA ATG CAA AAA TTT ACT GCC AAG ATT GTC AAT ATG 604  
139 Ser Phe Arg Thr Asp Asn Gly Pro Phe Lys Ala Ala Met Gln Lys Phe Thr Ala Lys Ile Val Asn Met 161

605 ATG AAA GCG GAA CGT TTG TAT GAA ACT CAA GGG GGG CCA ATA ATT TTA TCT CAG ATT GAG AAT GAA TAT 673  
162 Met Lys Ala Glu Arg Leu Tyr Glu Thr Gln Gly Gly Pro Ile Ile Leu Ser Gln Ile Glu Asn Glu Tyr 184

674 GGA CCC ATG GAA TGG GAA CTG GGA GCA CCA GGT AAA TCT TAC GCA CAG TGG GCC GCC AAA ATG GCT GTG 742  
185 Gly Pro Met Glu Trp Glu Leu Gly Ala Pro Gly Lys Ser Tyr Ala Gln Trp Ala Ala Lys Met Ala Val 207

743 GGT CTT GAC ACT GGT GTC CCA TGG GTT ATG TGC AAG CAA GAC GAT GCC CCT GAT CCT ATT ATA AAT GCT 811  
208 Gly Leu Asp Thr Gly Val Pro Trp Val Met Cys Lys Gln Asp Asp Ala Pro Asp Pro Ile Ile Asn Ala 230

812 TGC AAT GGC TTC TAC TGT GAC TAC TTT TCT CCA AAC AAG GCT TAT AAA CCA AAG ATA TGG ACT GAA GCC 880  
231 Cys Asn Gly Phe Tyr Cys Asp Tyr Phe Ser Pro Asn Lys Ala Tyr Lys Pro Lys Ile Trp Thr Glu Ala 253

881 TGG ACT GCA TGG TTT ACT GGT TTT GGA AAT CCA GTT CCT TAC CGT CCT GCT GAG GAC TTG GCA TTT TCT 949  
254 Trp Thr Ala Trp Phe Thr Gly Phe Gly Asn Pro Val Pro Tyr Arg Pro Ala Glu Asp Leu Ala Phe Ser 276

950 GTT GCA AAA TTT ATA CAG AAG GGA GGT TCC TTC ATC AAT TAT TAC ATG TAT CAT GGA GGA ACA AAC TTT 1018  
277 Val Ala Lys Phe Ile Gln Lys Gly Gly Ser Phe Ile Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe 299

1019 GGA CGG ACT GCT GGT GGT CCA TTT ATT GCT ACT AGT TAT GAC TAT GAT GCA CCA CTT GAT GAA TAT GGA 1087  
300 Gly Arg Thr Ala Gly Gly Pro Phe Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Tyr Gly 322

1088 TTA TTG CGA CAA CCA AAA TGG GGT CAC CTG AAA GAT CTG CAT AGA GCA ATA AAG CTT TGT GAA CCA GCT 1156  
323 Leu Leu Arg Gln Pro Lys Trp Gly His Leu Lys Asp Leu His Arg Ala Ile Lys Leu Cys Glu Pro Ala 345

1157 TTA GTC TCT GGA GAT CCA GCT GTG ACA GCA CTT GGA CAC CAG CAG GAG GCC CAT GTT TTT AGG TCG AAG 1225  
346 Leu Val Ser Gly Asp Pro Ala Val Thr Ala Leu Gly His Gln Gln Glu Ala His Val Phe Arg Ser Lys 368

1226 GCT GGC TCT TGT GCT GCA TTC CTT GCT AAC TAC GAC CAA CAC TCT TTT GCT ACT GTG TCA TTT GCA AAC 1294  
369 Ala Gly Ser Cys Ala Ala Phe Leu Ala Asn Tyr Asp Gln His Ser Phe Ala Thr Val Ser Phe Ala Asn 391

1295 AGG CAT TAC AAC TTG CCA CCA TGG TCA ATC AGC ATT CTT CCC GAC TGC AAG AAC ACT GTA TTT AAT ACA 1363  
392 Arg His Tyr Asn Leu Pro Pro Trp Ser Ile Ser Ile Leu Pro Asp Cys Lys Asn Thr Val Phe Asn Thr 414

1364 GCA CGG ATC GGT GCT CAA AGT GCT CAG ATG AAG ATG ACT CCA GTC AGC AGA GGA TTG CCC TGG CAG TCA 1432  
415 Ala Arg Ile Gly Ala Gln Ser Ala Gln Met Lys Met Thr Pro Val Ser Arg Gly Leu Pro Trp Gln Ser 437

1433 TTC AAT GAA GAG ACA TCA TCT TAT GAA GAC AGT AGT TTT ACA GTT GTT GGG CTA TTG GAA CAG ATA AAT 1501  
438 Phe Asn Glu Glu Thr Ser Ser Tyr Glu Asp Ser Ser Phe Thr Val Val Gly Leu Leu Glu Gln Ile Asn 460

0005 0307 0/ 031109 0'008 852

Figure 2  
She 16 of 12

Gene/clone name: TB03/p2-1-3/b1; accession number AF154421; Sequence ID number 3 cont.



1502	ACA ACA AGA GAC GTG TCT GAT TAT TTG TGG TAT TCA ACA GAT GTC AAG ATT GAT TCA AGA GAA AAG TTT	1570
461	Thr Thr Arg Asp Val Ser Asp Tyr Leu Trp Tyr Ser Thr Asp Val Lys Ile Asp Ser Arg Glu Lys Phe	483
1571	TTG AGA GGC GGA AAA TGG CCT TGG CTT ACG ATC ATG TCA GCT GGG CAT GCA TTG CAT GTT TTT GTG AAT	1639
484	Leu Arg Gly Gly Lys Trp Pro Trp Leu Thr Ile Met Ser Ala Gly His Ala Leu His Val Phe Val Asn	506
1640	GGT CAA TTA GCA GGA ACT GCA TAT GGA AGT TTA GAA AAA CCG AAA CTA ACT TTC AGT AAA GCC GTA AAT	1708
507	Gly Gln Leu Ala Gly Thr Ala Tyr Gly Ser Leu Glu Lys Pro Lys Leu Thr Phe Ser Lys Ala Val Asn	529
1709	CTG AGA GCA GGT GTT AAC AAG ATT TCT CTA CTG AGC ATT GCT GTT GGC CTT CCG AAT ATC GGC CCA CAT	1777
530	Leu Arg Ala Gly Val Asn Lys Ile Ser Leu Leu Ser Ile Ala Val Gly Leu Pro Asn Ile Gly Pro His	552
1778	TTT GAG ACA TGG AAT GCT GGT GTT CTT GGG CCA GTC TCA CTA ACT GGT CTT GAC GAG GGG AAA AGA GAT	1846
553	Phe Glu Thr Trp Asn Ala Gly Val Leu Gly Pro Val Ser Leu Thr Gly Leu Asp Glu Gly Lys Arg Asp	575
1847	TTA ACA TGG CAG AAA TGG TCT TAC AAG GTT GGT CTA AAA GGA GAA GCC TTG AGC CTC CAT TCA CTC AGT	1915
576	Leu Thr Trp Gln Lys Trp Ser Tyr Lys Val Gly Leu Lys Gly Glu Ala Leu Ser Leu His Ser Leu Ser	598
1916	GGT AGC TCG TCA GTT GAG TGG GTC GAG GGT TCT TTA GTG GCT CAG AGA CAG CCA CTC ACA TGG TAC AAG	1984
599	Gly Ser Ser Ser Val Glu Trp Val Glu Gly Ser Leu Val Ala Gln Arg Gln Pro Leu Thr Trp Tyr Lys	621
1985	AGC ACT TTT AAT GCT CCA GCT GGA AAT GAT CCT TTG GCT TTA GAC TTG AAT ACC ATG GGC AAA GGA CAA	2053
622	Ser Thr Phe Asn Ala Pro Ala Gly Asn Asp Pro Leu Ala Leu Asp Leu Asn Thr Met Gly Lys Gly Gln	644
2054	GTG TGG ATA AAT GGT CAA AGC CTC GGA CGC TAT TGG CCT GGA TAT AAA GCA TCT GGT AAC TGC GGT GCC	2122
645	Val Trp Ile Asn Gly Gln Ser Leu Gly Arg Tyr Trp Pro Gly Tyr Lys Ala Ser Gly Asn Cys Gly Ala	667
2123	TGT AAC TAT GCA GGC TGG TTT AAT GAG AAA AAA TGC CTA AGT AAC TGT GGA GAG GCT TCA CAA CGA TGG	2191
668	Cys Asn Tyr Ala Gly Trp Phe Asn Glu Lys Lys Cys Leu Ser Asn Cys Gly Glu Ala Ser Gln Arg Trp	690
2192	TAT CAT GTT CCC CGT TCT TGG CTG TAT CCT ACT GGA AAT TTG TTA GTT CTA TTT GAG GAA TGG GGA GGA	2260
691	Tyr His Val Pro Arg Ser Trp Leu Tyr Pro Thr Gly Asn Leu Leu Val Leu Phe Glu Glu Trp Gly Gly	713
2261	GAG CCT CAT GGA ATC TCT TTG GTA AAA AGA GAA GTT GCA AGT GTT TGT GCA GAT ATA AAC GAA TGG CAA	2329
714	Glu Pro His Gly Ile Ser Leu Val Lys Arg Glu Val Ala Ser Val Cys Ala Asp Ile Asn Glu Trp Gln	736
2330	CCA CAG TTG GTG AAT TGG CAA ATG CAA GCA TCT GGT AAA GTT GAC AAA CCA CTG AGA CCT AAA GCT CAC	2398
737	Pro Gln Leu Val Asn Trp Gln Met Gln Ala Ser Gly Lys Val Asp Lys Pro Leu Arg Pro Lys Ala His	759
2399	CTC TCG TGT GCT TCT GGT CAG AAG ATT ACT TCA ATC AAA TTT GCA AGC TTT GGA ACA CCA CAA GGG GTC	2467
760	Leu Ser Cys Ala Ser Gly Gln Lys Ile Thr Ser Ile Lys Phe Ala Ser Phe Gly Thr Pro Gln Gly Val	782
2468	TGC GGA AGC TTC CGT GAA GGA AGC TGC CAC GCC TTC CAC TCA TAT GAT GCT TTT GAA AGG TAT TGC ATC	2536
783	Cys Gly Ser Phe Arg Glu Gly Ser Cys His Ala Phe His Ser Tyr Asp Ala Phe Glu Arg Tyr Cys Ile	805
2537	GGG CAA AAC TCG TGC TCA GTA CCT GTA ACA CCA GAG ATC TTT GGA GGT GAT CCA TGT CCA CAT GTT ATG	2605
806	Gly Gln Asn Ser Cys Ser Val Pro Val Thr Pro Glu Ile Phe Gly Gly Asp Pro Cys Pro His Val Met	828
2606	AAG AAA CTC TCA GTT GAG GTT ATT TGC AGT TGA TGACACTGAGGAGAAACAAATAAAAGTGGTTTCAGTTAGTTGTCTGAA	2686
829	Lys Lys Leu Ser Val Glu Val Ile Cys Ser ***	840
2687	CATATCAAAAAGTTGGCTTTGATGGAGGTGAAGTTGTACAGATATGCAACACACCTTTCCATTTGAGGCACATATGAATTGCAATGGCCCAA	2778
2779	GATTCTGTACATATATGTTGGTTACTGTCAAGTTGGTATTGGTTTGCAAAATGTAACACAGTAGTATAGTCATTGGTTCAAGTGCCGATCGAG	2870
2871	ATTGTGCTAGTGGGAGTAGTAGGTACCGATCGATCTATCGTTGTTTGCAACAAGCTGGCCCTAGATTCCACTATTATTATAACAAAGAAAGC	2962
2963	ACAATGAGACTGATTCTTGATTAGTCCATGTGTAGATATTGTTACTGTTGGAATTTGCAAAATCTTGTGATTTTCAGCAAAAAAAAAAAAAA	3054
3055	AAAAAAAAAAAAA	3069

Figure 2  
Sheet 7 of 12

one/clone name: TBG4/pzBG2-~~1~~pTombgal4; accession number AF02035 Sequence ID number 4

1	AAAAAAGTTTCAATTTTTTTTCTAAATAAAAAAATTCATTTTTTTGAATGTGGAAAAA	63
64	ATG CTA AGG ACT AAT GTG TTG TTG TTA TTA GTT ATT TGT TTA TTG GAT TTT TTT TCT TCA GTG AAA GCT	132
1	Met Leu Arg Thr Asn Val Leu Leu Leu Leu Val Ile Cys Leu Leu Asp Phe Phe Ser Ser Val Lys Ala	23
133	AGT GTT TCT TAT GAT GAC AGA GCT ATA ATC ATA AAT GGG AAA AGA AAA ATT CTT ATT TCT GGT TCA ATT	201
24	Ser Val Ser Tyr Asp Asp Arg Ala Ile Ile Ile Asn Gly Lys Arg Lys Ile Leu Ile Ser Gly Ser Ile	46
202	CAT TAT CCA AGA AGC ACT CCA CAG ATG TGG CCT GAT CTT ATA CAA AAG GCT AAA GAT GGA GGC TTA GAT	270
47	His Tyr Pro Arg Ser Thr Pro Gln Met Trp Pro Asp Leu Ile Gln Lys Ala Lys Asp Gly Gly Leu Asp	69
271	GTT ATT GAA ACT TAT GTT TTC TGG AAT GGA CAT GAG CCT TCT CCT GGA AAA TAT AAT TTT GAA GGA AGA	339
70	Val Ile Glu Thr Tyr Val Phe Trp Asn Gly His Glu Pro Ser Pro Gly Lys Tyr Asn Phe Glu Gly Arg	92
340	TAT GAT CTT GTT AGA TTC ATC AAA ATG GTA CAA AGA GCA GGA CTT TAT GTC AAT TTA CGT ATT GGC CCT	408
93	Tyr Asp Leu Val Arg Phe Ile Lys Met Val Gln Arg Ala Gly Leu Tyr Val Asn Leu Arg Ile Gly Pro	115
409	TAC GTC TGT GCT GAA TGG AAC TTT GGG GGA TTC CCT GTT TGG CTA AAA TAT GTG CCT GGT ATG GAA TTT	477
116	Tyr Val Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro Gly Met Glu Phe	138
478	AGA ACA AAC AAT CAG CCT TTT AAG GTG GCT ATG CAA GGA TTT GTT CAG AAA ATA GTC AAC ATG ATG AAG	546
139	Arg Thr Asn Asn Gln Pro Phe Lys Val Ala Met Gln Gly Phe Val Gln Lys Ile Val Asn Met Met Lys	161
547	TCA GAA AAT TTG TTT GAA TCT CAA GGA GGA CCA ATA ATT ATG GCC CAG ATA GAA AAT GAG TAT GGA CCA	615
162	Ser Glu Asn Leu Phe Glu Ser Gln Gly Gly Pro Ile Ile Met Ala Gln Ile Glu Asn Glu Tyr Gly Pro	184
616	GTA GAA TGG GAA ATT GGT GCT CCT GGT AAA GCT TAT ACA AAA TGG GCA GCT CAA ATG GCT GTA GGT TTG	684
185	Val Glu Trp Glu Ile Gly Ala Pro Gly Lys Ala Tyr Thr Lys Trp Ala Ala Gln Met Ala Val Gly Leu	207
685	AAA ACT GGT GTC CCA TGG ATC ATG TGT AAG CAA GAG GAT GCT CCT GAT CCT GTG ATT GAT ACT TGT AAT	753
208	Lys Thr Gly Val Pro Trp Ile Met Cys Lys Gln Glu Asp Ala Pro Asp Pro Val Ile Asp Thr Cys Asn	230
754	GGC TTC TAC TGC GAA GGG TTC CGT CCT AAT AAG CCT TAC AAA CCT AAA ATG TGG ACA GAA GTA TGG ACT	822
231	Gly Phe Tyr Cys Glu Gly Phe Arg Pro Asn Lys Pro Tyr Lys Pro Lys Met Trp Thr Glu Val Trp Thr	253
823	GGC TGG TAT ACG AAA TTC GGT GGT CCA ATT CCT CAA AGA CCA GCC GAA GAC ATT GCA TTT TCA GTT GCC	891
254	Gly Trp Tyr Thr Lys Phe Gly Gly Pro Ile Pro Gln Arg Pro Ala Glu Asp Ile Ala Phe Ser Val Ala	276
892	AGG TTT GTT CAG AAC AAT GGT TCA TTC TTC AAT TAC TAC ATG TAT CAT GGA GGA ACA AAT TTT GGC CGG	960
277	Arg Phe Val Gln Asn Asn Gly Ser Phe Phe Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly Arg	299
961	ACA TCA TCA GGG CTT TTC ATT GCA ACT AGC TAC GAT TAT GAT GCT CCT CTC GAT GAA TAT GGG TTG CTG	1029
300	Thr Ser Ser Gly Leu Phe Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Tyr Gly Leu Leu	322
1030	AAT GAA CCA AAG TAT GGG CAC TTG AGA GAC TTA CAT AAA GCT ATC AAG CTA TCT GAA CCG GCT TTA GTT	1098
323	Asn Glu Pro Lys Tyr Gly His Leu Arg Asp Leu His Lys Ala Ile Lys Leu Ser Glu Pro Ala Leu Val	345
1099	TCA TCA TAT GCT GCG GTG ACT AGT CTT GGA AGT AAT CAA GAG GCT CAT GTT TAT AGA TCA AAA TCT GGA	1167
346	Ser Ser Tyr Ala Ala Val Thr Ser Leu Gly Ser Asn Gln Glu Ala His Val Tyr Arg Ser Lys Ser Gly	368
1168	GCT TGT GCT GCT TTT TTA TCC AAC TAT GAC TCT AGA TAT TCA GTA AAA GTC ACC TTT CAG AAT AGG CCA	1236
369	Ala Cys Ala Ala Phe Leu Ser Asn Tyr Asp Ser Arg Tyr Ser Val Lys Val Thr Phe Gln Asn Arg Pro	391
1237	TAC AAT CTG CCT CCA TGG TCC ATC AGC ATT CTT CCC GAC TGC AAA ACT GCC GTT TAC AAC ACT GCA CAG	1305
392	Tyr Asn Leu Pro Pro Trp Ser Ile Ser Ile Leu Pro Asp Cys Lys Thr Ala Val Tyr Asn Thr Ala Gln	414
1306	GTT AAC TCT CAA AGC TCG AGC ATA AAG ATG ACG CCT GCA GGT GGT GGA TTG TCT TGG CAG TCA TAC AAT	1374
415	Val Asn Ser Gln Ser Ser Ser Ile Lys Met Thr Pro Ala Gly Gly Gly Leu Ser Trp Gln Ser Tyr Asn	437
1375	GAA GAA ACG CCT ACT GCT GAT GAC AGC GAT ACA CTT ACA GCT AAC GGA CTA TGG GAA CAG AAA AAC GTC	1443
438	Glu Glu Thr Pro Thr Ala Asp Asp Ser Asp Thr Leu Thr Ala Asn Gly Leu Trp Glu Gln Lys Asn Val	460



Figure 2  
Sheet 8 of 12Gene/clone name: TBG4/pZBG2-/pTomβgal4; accession number AF0203 Sequence ID number 4  
cont.

1444	ACA AGA GAT TCA TCA GAC TAT CTG TGG TAC ATG ACA AAT GTA AAT ATA GCA TCT AAT GAA GGA TTT CTA	1512
461	Thr Arg Asp Ser Ser Asp Tyr Leu Trp Tyr Met Thr Asn Val Asn Ile Ala Ser Asn Glu Gly Phe Leu	483
1513	AAG AAC GGA AAG GAT CCT TAT CTC ACT GTT ATG TCC GCT GGT CAT GTC TTG CAT GTT TTC GTC AAT GGA	1581
484	Lys Asn Gly Lys Asp Pro Tyr Leu Thr Val Met Ser Ala Gly His Val Leu His Val Phe Val Asn Gly	506
1582	AAA CTA TCA GGA ACT GTT TAT GGT ACA TTG GAT AAT CCA AAA CTT ACA TAC AGT GGC AAC GTG AAG TTA	1650
507	Lys Leu Ser Gly Thr Val Tyr Gly Thr Leu Asp Asn Pro Lys Leu Thr Tyr Ser Gly Asn Val Lys Leu	529
1651	AGA GCT GGT ATT AAC AAG ATT TCT CTG CTC AGT GTT TCC GTT GGT CTC CCG AAC GTT GGC GTG CAT TAT	1719
530	Arg Ala Gly Ile Asn Lys Ile Ser Leu Leu Ser Val Ser Val Gly Leu Pro Asn Val Gly Val His Tyr	552
1720	GAT ACA TGG AAT GCA GGA GTT CTA GGT CCA GTC ACG TTG AGC GGT CTC AAT GAA GGG TCA AGA AAC TTG	1788
553	Asp Thr Trp Asn Ala Gly Val Leu Gly Pro Val Thr Leu Ser Gly Leu Asn Glu Gly Ser Arg Asn Leu	575
1789	GCG AAA CAG AAA TGG TCT TAC AAG GTT GGT CTG AAA GGC GAA TCG TTA AGT CTT CAC TCC TTA AGT GCG	1857
576	Ala Lys Gln Lys Trp Ser Tyr Lys Val Gly Leu Lys Gly Glu Ser Leu Ser Leu His Ser Leu Ser Gly	598
1858	AGT TCT TCT GTT GAA TGG GTT CGA GGT TCA CTA ATG GCT CAA AAG CAG CCC CTG ACT TGG TAC AAG GCT	1926
599	Ser Ser Ser Val Glu Trp Val Arg Gly Ser Leu Met Ala Gln Lys Gln Pro Leu Thr Trp Tyr Lys Ala	621
1927	ACA TTT AAC GCG CCT GGA GGA AAT GAT CCA CTA GCT TTA GAC ATG GCA AGT ATG GGA AAA GGT CAG ATA	1995
622	Thr Phe Asn Ala Pro Gly Gly Asn Asp Pro Leu Ala Leu Asp Met Ala Ser Met Gly Lys Gly Gln Ile	644
1996	TGG ATA AAT GGT GAA GGC GTA GGT CGC CAT TGG CCT GGA TAC ATA GCA CAA GGC GAC TGC AGC AAA TGC	2064
645	Trp Ile Asn Gly Glu Gly Val Gly Arg His Trp Pro Gly Tyr Ile Ala Gln Gly Asp Cys Ser Lys Cys	667
2065	AGT TAT GCT GGA ACG TTC AAC GAG AAG AAG TGC CAG ACT AAC TGC GGA CAA CCT TCT CAG AGA TGG TAC	2133
668	Ser Tyr Ala Gly Thr Phe Asn Glu Lys Lys Cys Gln Thr Asn Cys Gly Gln Pro Ser Gln Arg Trp Tyr	690
2134	CAT GTT CCA CGA TCG TGG CTG AAA CCA AGT GGA AAC TTG TTA GTA GTA TTC GAA GAA TGG GGA GGT AAT	2202
691	His Val Pro Arg Ser Trp Leu Lys Pro Ser Gly Asn Leu Leu Val Val Phe Glu Glu Trp Gly Gly Asn	713
2203	CCA ACA GGA ATT TCT CTA GTC AGG AGA TCA AGA TAA AGAACTCGAAAAGTAAACCTTGTTTCAGTAAGTATGGTGTGAA	2282
714	Pro Thr Gly Ile Ser Leu Val Arg Arg Ser Arg ***	725
2283	TTGCGCGCCGAAAAATACATACACGAAGCTAACAATGGAGGCTACAGTTTGCAAAATTGCAGCTGAATAAAACATTAGAAGATAAAGAAATATT	2374
2375	TGATTAAAAGGAGTATATAAATTTACAGAGAATTTTCTTTATTCCTTTGTAAACCTTTGGTTTATAAAGTTTATACAGAATTTTCGTGTTATTT	2466
2467	GGATTATGAGATTGAAGAAGATTGTACAGCTTCCAAATACTATTAGAATACAAATAAATTTTCATGTAAAAA	2554

Figure 2  
Sh 19 of 12

Gene/clone name: TBG5/RT2-1/b1; accession number AF154423; sequence ID number 5

1 ATC CAG ACT TAC GTT TTC TGG AAC CTT CAT GAA CCT GTT CGA AAT CAG TAT GAT TTT GAA GGA AGG AAA 69  
1 Ile Gln Thr Tyr Val Phe Trp Asn Leu His Glu Pro Val Arg Asn Gln Tyr Asp Phe Glu Gly Arg Lys 23

70 GAT TTG ATT AAT TTT GTG AAG TTG GTG GAG AGA GCT GGC TTA TTT GTT CAT ATA AGG ATT GGG CCT TAT 138  
24 Asp Leu Ile Asn Phe Val Lys Leu Val Glu Arg Ala Gly Leu Phe Val His Ile Arg Ile Gly Pro Tyr 46

139 GTT TGT GCA GAA TGG AAC TAT GGT GGG TTT CCT CTT TGG TTG CAT TTC ATT CCT GGA ATT GAA TTT CGA 207  
47 Val Cys Ala Glu Trp Asn Tyr Gly Gly Phe Pro Leu Trp Leu His Phe Ile Pro Gly Ile Glu Phe Arg 69

208 ACC GAC AAT GAA CCG TTC AAG GCA GAA ATG AAG CGA TTC ACA GCT AAA ATT GTT GAC ATG ATC AAG CAA 276  
70 Thr Asp Asn Glu Pro Phe Lys Ala Glu Met Lys Arg Phe Thr Ala Lys Ile Val Asp Met Ile Lys Gln 92

277 GAA AAT CTA TAT GCA TCC CAG GGT GGG CCG GTT ATC TTG TCT CAG ATA GAA AAT GAG TAT GGC AAT GGT 345  
93 Glu Asn Leu Tyr Ala Ser Gln Gly Gly Pro Val Ile Leu Ser Gln Ile Glu Asn Glu Tyr Gly Asn Gly 115

346 GAT ATT GAG TCT CGT TAT GGT CCT CGT GCC AAA CCT TAC GTG AAC TGG GCA GCA TCA ATG GCT ACG TCT 414  
116 Asp Ile Glu Ser Arg Tyr Gly Pro Arg Ala Lys Pro Tyr Val Asn Trp Ala Ala Ser Met Ala Thr Ser 138

415 TTA AAT ACG GGA GTG CCA TGG GTT ATG TGT CAG CAA CCA GAT GCC CCT CCT TCC GTT ATT AAC ACT TGC 483  
139 Leu Asn Thr Gly Val Pro Trp Val Met Cys Gln Gln Pro Asp Ala Pro Pro Ser Val Ile Asn Thr Cys 161

484 AAT GGA TTT TAT TGT GAC CAA TTC AAG CAA AAT TCC GAT AAA ACA CCC AAG ATG TGG ACT GAG AAT TGG 552  
162 Asn Gly Phe Tyr Cys Asp Gln Phe Lys Gln Asn Ser Asp Lys Thr Pro Lys Met Trp Thr Glu Asn Trp 184

553 ACC GGA TGG TTT CTG TGG TTT GGT GGT CCT GTC CCT TAC AGA CCA GTG GAA GAC ATC GCT TTC GCT GTG 621  
185 Thr Gly Trp Phe Leu Ser Phe Gly Gly Pro Val Pro Tyr Arg Pro Val Glu Asp Ile Ala Phe Ala Val 207

622 GCT CGA TTT TTC CAG CGA GGC GGA ACT TTC CAG AAC TAT TAC ATG TAC CAC GGG GGA ACT AAC TTT GGG 690  
208 Ala Arg Phe Phe Gln Arg Gly Gly Thr Phe Gln Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly 230

691 AGA ACC AGT GGT GGA CCG TTT ATT GCA ACT AGC TAT GAC TAT GAT GCC CCT CTC GAC GAA TAC GG 755  
231 Arg Thr Ser Gly Gly Pro Phe Ile Ala Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Asp Glu Tyr 252

Figure 2  
Sheet 10 of 12

Gene/clone name: TBG6/RT-2-6/b1; accession number AF154424; Sequence ID number 5

1	ATC	CAG	ACA	TAT	GTT	TTT	TGG	AAT	GTT	CAT	GAG	CCT	TCT	CCT	GGC	AAT	TAC	AAT	TTT	GAA	GGA	AGA	TAT	69
1	Ile	Gln	Thr	Tyr	Val	Phe	Trp	Asn	Val	His	Glu	Pro	Ser	Pro	Gly	Asn	Tyr	Asn	Phe	Glu	Gly	Arg	Tyr	23
70	GAC	CTG	GTG	AGG	TTT	GTA	AAA	ACG	ATT	CAG	AAA	GCA	GGG	CTG	TAT	GCT	CAT	CIT	CGA	ATT	GGC	CCT	TAC	138
24	Asp	Leu	Val	Arg	Phe	Val	Lys	Thr	Ile	Gln	Lys	Ala	Gly	Leu	Tyr	Ala	His	Leu	Arg	Ile	Gly	Pro	Tyr	46
139	GTT	TGT	GCA	GAG	TGG	AAT	TTT	GGA	GGG	TTT	CCA	GTA	TGG	CTG	AAG	TAT	GTA	CCT	GGC	ATT	AGC	TTC	AGA	207
47	Val	Cys	Ala	Glu	Trp	Asn	Phe	Gly	Gly	Phe	Pro	Val	Trp	Leu	Lys	Tyr	Val	Pro	Gly	Ile	Ser	Phe	Arg	69
208	GCT	GAT	AAT	GAA	CCT	TTC	AAG	AAC	GCA	ATG	AAA	GGG	TAT	GCT	GAG	AAA	ATT	GTT	AAC	TTG	ATG	AAG	ATC	276
70	Ala	Asp	Asn	Glu	Pro	Phe	Lys	Asn	Ala	Met	Lys	Gly	Tyr	Ala	Glu	Lys	Ile	Val	Asn	Leu	Met	Lys	Ile	92
277	ATA	ATC	TTT	TCG	AGT	CTC	AGG	GTG	GTC	CAA	TCA	TAC	TCT	CAC	AGA	TTG	AGA	ATG	AGT	ATG	GGC	CTC	AAG	345
93	Ile	Ile	Phe	Ser	Ser	Leu	Arg	Val	Val	Gln	Ser	Tyr	Ser	His	Arg	Leu	Arg	Met	Ser	Met	Gly	Leu	Lys	115
346	CCA	AGG	TAC	TTG	GAG	CAC	CGG	GAC	ATC	AGT	ATT	CAA	CAT	GGG	CTG	CAA	ATA	TGG	CAG	TTG	GAT	TTG	AAC	414
116	Pro	Arg	Tyr	Leu	Glu	His	Arg	Asp	Ile	Ser	Ile	Gln	His	Gly	Leu	Gln	Ile	Trp	Gln	Leu	Asp	Leu	Asn	138
415	ACA	GGC	GTC	CCA	TGG	GTG	ATG	TGC	AAG	GAA	GAA	GAT	GCA	CCA	GAT	CCT	GTG	ATC	AAC	ACA	TGC	AAT	GGT	483
139	Thr	Gly	Val	Pro	Trp	Val	Met	Cys	Lys	Glu	Glu	Asp	Ala	Pro	Asp	Pro	Val	Ile	Asn	Thr	Cys	Asn	Gly	161
484	TTC	TAC	TGT	GAT	AAT	TTC	TTC	CCA	AAC	AAA	CCA	TAC	AAA	CCT	GCA	ATT	TGG	ACT	GAA	GCT	TGG	AGT	GGA	552
162	Phe	Tyr	Cys	Asp	Asn	Phe	Phe	Pro	Asn	Lys	Pro	Tyr	Lys	Pro	Ala	Ile	Trp	Thr	Glu	Ala	Trp	Ser	Gly	184
553	TGG	TTC	TCG	GAA	TTT	GGC	GGT	CCC	CTT	CAT	CAG	AGA	CCA	GTT	CAG	GAT	TTG	GCA	TTT	GCT	GTT	GCC	CAA	621
185	Trp	Phe	Ser	Glu	Phe	Gly	Gly	Pro	Leu	His	Gln	Arg	Pro	Val	Gln	Asp	Leu	Ala	Phe	Ala	Val	Ala	Gln	207
622	TTT	ATA	CAA	AGA	GGA	GGA	TCT	TIT	GTT	AAC	TAT	TAC	ATG	TAC	CAT	GGG	GGC	ACG	AAC	TTT	GGA	CGC	ACT	690
208	Phe	Ile	Gln	Arg	Gly	Gly	Ser	Phe	Val	Asn	Tyr	Tyr	Met	Tyr	His	Gly	Gly	Thr	Asn	Phe	Gly	Arg	Thr	230
691	GGG	GGT	GGG	CCA	TTC	ATC	ACT	ACC	AGC	TAT	GAT	TAT	GAT	CCC	CCC	CTC	GAC	GAG	TAT	GG				749
231	Ala	Gly	Gly	Pro	Phe	Ile	Thr	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Leu	Asp	Glu	Tyr					250

12/31

Figure 2  
Sheet 11 of 12

Gene/clone name: TBG7/22-1-18; accession number AF154422; sequence number 7

		GCNACCTCTCTGCA		12
1	13	GTGAATAACACCGGTAAACGGCCAATGCCAACTCTCGTCGGAATCTGAATAGTGATTAAAGCAGCTTAGCTAGCTAACTTTTGCCTCTGCA		103
104	1	ATG AAC ACA ATG AGT TGT TTG TCC TCT AAT TTC AAG TTC GTT TTC CTT GCC TCG ACT GTG ATA TGG ATG		172
	1	Met Asn Thr Met Ser Cys Leu Ser Ser Asn Phe Lys Phe Val Phe Leu Ala Ser Thr Val Ile Trp Met		23
173		ACG GTA ATG TCG TCG TCG TTA GCA GCA GTA GAT GCT TCC AAT GTT ACT ACT ATT GGT ACT GAT AGT GTG		241
	24	Thr Val Met Ser Ser Ser Leu Ala Ala Val Asp Ala Ser Asn Val Thr Thr Ile Gly Thr Asp Ser Val		46
242		ACT TAC GAT CGA CGC TCG TTG ATT ATT AAC GGC CAG AGG AAG CTG CTC ATC TCC GCT TCC ATT CAC TAT		310
	47	Thr Tyr Asp Arg Arg Ser Leu Ile Ile Asn Gly Gln Arg Lys Leu Leu Ile Ser Ala Ser Ile His Tyr		69
311		CCT CGC AGT GTC CCT GCC ATG TGG CCT GGT CTG GTT CGA TTG GCG AAG GAA GGA GGA GTG GAT GTT ATT		379
	70	Pro Arg Ser Val Pro Ala Met Trp Pro Gly Leu Val Arg Leu Ala Lys Glu Gly Gly Val Asp Val Ile		92
380		GAA ACG TAT GTT TTC TGG AAC GGT CAC GAA CCT TCT CCG GGC AAT TAT TAC TTT GGA GGA AGG TTT GAT		448
	93	Glu Thr Tyr Val Phe Trp Asn Gly His Glu Pro Ser Pro Gly Asn Tyr Tyr Phe Gly Gly Arg Phe Asp		115
449		CTA GTC AAA TTT TGT AAG ATC ATT CAG CAG GCT GGA ATG TAT ATG ATT CTT CGG ATT GGA CCA TTT GTA		517
	116	Leu Val Lys Phe Cys Lys Ile Ile Gln Gln Ala Gly Met Tyr Met Ile Leu Arg Ile Gly Pro Phe Val		138
518		GCT GCA GAA TGG AAC TTT GGT GGA CTT CCT GTG TGG TTG CAT TAT GTG CCA GGT ACC ACC TTT CGG ACT		586
	139	Ala Ala Glu Trp Asn Phe Gly Gly Leu Pro Val Trp Leu His Tyr Val Pro Gly Thr Thr Phe Arg Thr		161
587		GAT AGT GAA CCA TTT AAG TAT CAC ATG CAG AAG TTC ATG ACA TAT ACA GTG AAC TTA ATG AAG AGA GAG		655
	162	Asp Ser Glu Pro Phe Lys Tyr His Met Gln Lys Phe Met Thr Tyr Thr Val Asn Leu Met Lys Arg Glu		184
656		AGG CTT TTT GCA TCT CAA GGA GGT CCA ATC ATC TTG TCA CAG GTA GAA AAT GAG TAC GGC TAC TAT GAA		724
	185	Arg Leu Phe Ala Ser Gln Gly Gly Pro Ile Ile Leu Ser Gln Val Glu Asn Glu Tyr Gly Tyr Tyr Glu		207
725		AAT GCA TAT GGA GAA GGA GGG AAA AGG TAT GCC TTA TGG GCT GCT AAA ATG GCC CTT TCT CAA AAT ACT		793
	208	Asn Ala Tyr Gly Glu Gly Gly Lys Arg Tyr Ala Leu Trp Ala Ala Lys Met Ala Leu Ser Gln Asn Thr		230
794		GGT GTA CCT TGG ATA ATG TGC CAG CAG TAT GAT GCT CCT GAT CCT GTG ATT GAC ACA TGC AAT TCA TTT		862
	231	Gly Val Pro Trp Ile Met Cys Gln Gln Tyr Asp Ala Pro Asp Pro Val Ile Asp Thr Cys Asn Ser Phe		253
863		TAC TGC GAC CAA TTT AAA CCA ATC TCT CCA AAC AAG CCC AAA ATT TGG ACA GAG AAC TGG CCG GGA TGG		931
	254	Tyr Cys Asp Gln Phe Lys Pro Ile Ser Pro Asn Lys Pro Lys Ile Trp Thr Glu Asn Trp Pro Gly Trp		276
932		TTC AAG ACA TTT GGG GCC AGA GAT CCT CAC AGG CCT GCA GAA GAT GTT GCT TAT TCC GTG GCT CGT TTT		1000
	277	Phe Lys Thr Phe Gly Ala Arg Asp Pro His Arg Pro Ala Glu Asp Val Ala Tyr Ser Val Ala Arg Phe		299
1001		TTC CAA AAA GGA GGA AGC GTG CAG AAT TAT TAC ATG TAC CAT GGT GGG ACG AAC TTT GGC AGG ACA GCA		1069
	300	Phe Gln Lys Gly Gly Ser Val Gln Asn Tyr Tyr Met Tyr His Gly Gly Thr Asn Phe Gly Arg Thr Ala		322
1070		GGT GGC CCT TTC ATT ACC ACA AGT TAT GAC TAT GAT GCC CCA ATT GAC GAA TAT GGT TTA CCA AGG TTT		1138
	323	Gly Gly Pro Phe Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Asp Glu Tyr Gly Leu Pro Arg Phe		345
1139		CCA AAA TGG GGT CAC CTT AAA GAA CTT CAT AAA GTC ATA AAA TCG TGT GAG CAT GCT CTG CTG AAC AAT		1207
	346	Pro Lys Trp Gly His Leu Lys Glu Leu His Lys Val Ile Lys Ser Cys Glu His Ala Leu Leu Asn Asn		368
1208		GAT CCA ACT CTT CTT TCA TTA GGT CCT CTA CAA GAG GCT GAT GTT TAT GAA GAT GCT TCA GGC GCT TGT		1276
	369	Asp Pro Thr Leu Leu Ser Leu Gly Pro Leu Gln Glu Ala Asp Val Tyr Glu Asp Ala Ser Gly Ala Cys		391
1277		GCT GCC TTT CTC GCG AAT ATG GAT GAC AAA AAT GAC AAG GTG GTA CAG TTC CGA CAT GTA TCA TAC CAC		1345
	392	Ala Ala Phe Leu Ala Asn Met Asp Asp Lys Asn Asp Lys Val Val Gln Phe Arg His Val Ser Tyr His		414
1346		TTG CCA GCA TGG TCT GTT AGC ATT TTG CCA GAC TGC AAA AAT GTA GCG TTC AAC ACA GCA AAG GTT GGA		1414
	415	Leu Pro Ala Trp Ser Val Ser Ile Leu Pro Asp Cys Lys Asn Val Ala Phe Asn Thr Ala Lys Val Gly		437
1415		TGT CAA ACT TCT ATT GTC AAT ATG GCA CCC ATA GAT TTG CAT CCC ACC GCA AGT TCA CCA AAG AGA GAC		1483
	438	Cys Gln Thr Ser Ile Val Asn Met Ala Pro Ile Asp Leu His Pro Thr Ala Ser Ser Pro Lys Arg Asp		460

Figur 2  
Sheet 12 of 12

Gene/clone name: TBG7/pZBG-18; accession number AF154422; Sequence ID number 7 cont.

1484	ATC	AAG	TCT	CTT	CAG	TGG	GAA	GTC	TTC	AAG	GAA	ACA	GCT	GGA	GTA	TGG	GGA	GTT	GCT	GAT	TTC	ACT	AAA	1552
461	Ile	Lys	Ser	Leu	Gln	Trp	Glu	Val	Phe	Lys	Glu	Thr	Ala	Gly	Val	Trp	Gly	Val	Ala	Asp	Phe	Thr	Lys	483
1553	AAC	GGA	TTT	GTA	GAT	CAC	ATT	AAC	ACC	ACA	AAA	GAT	GCT	ACA	GAC	TAC	CTC	TGG	TAC	ACA	ACA	AGT	ATT	1621
484	Asn	Gly	Phe	Val	Asp	His	Ile	Asn	Thr	Thr	Lys	Asp	Ala	Thr	Asp	Tyr	Leu	Trp	Tyr	Thr	Thr	Ser	Ile	506
1622	TTT	GTT	CAT	GCA	GAG	GAG	GAT	TTC	CTA	AGA	AAC	AGA	GGC	ACT	GCA	ATG	CTT	TTC	GTT	GAA	TCA	AAG	GGT	1690
507	Phe	Val	His	Ala	Glu	Glu	Asp	Phe	Leu	Arg	Asn	Arg	Gly	Thr	Ala	Met	Leu	Phe	Val	Glu	Ser	Lys	Gly	529
1691	CAT	GCT	ATG	CAT	GTC	TTC	ATC	AAT	AAA	AAG	CTT	CAA	GCC	AGT	GCA	TCT	GGA	AAT	GGC	ACA	GTG	CCA	CAG	1759
530	His	Ala	Met	His	Val	Phe	Ile	Asn	Lys	Lys	Leu	Gln	Ala	Ser	Ala	Ser	Gly	Asn	Gly	Thr	Val	Pro	Gln	552
1760	TTC	AAG	TTT	GGA	ACT	CCT	ATT	GCT	CTA	AAG	GCA	GGG	AAG	AAT	GAA	ATT	TCC	TTG	TTA	AGC	ATG	ACT	GTG	1828
553	Phe	Lys	Phe	Gly	Thr	Pro	Ile	Ala	Leu	Lys	Ala	Gly	Lys	Asn	Glu	Ile	Ser	Leu	Leu	Ser	Met	Thr	Val	575
1829	GGC	CTA	CAA	ACA	GCT	GGA	GCG	TTT	TAT	GAA	TGG	ATT	GGA	GCT	GGT	CCA	ACA	AGT	GTC	AAA	GTT	GCA	GGG	1897
576	Gly	Leu	Gln	Thr	Ala	Gly	Ala	Phe	Tyr	Glu	Trp	Ile	Gly	Ala	Gly	Pro	Thr	Ser	Val	Lys	Val	Ala	Gly	598
1898	TTC	AAG	ACT	GGG	ACT	ATG	GAC	TTG	ACT	GCG	TCT	GCT	TGG	ACC	TAT	AAG	ATT	GGA	TTG	CAA	GGA	GAA	CAT	1966
599	Phe	Lys	Thr	Gly	Thr	Met	Asp	Leu	Thr	Ala	Ser	Ala	Trp	Thr	Tyr	Lys	Ile	Gly	Leu	Gln	Gly	Glu	His	621
1967	TTG	AGG	ATA	CAG	AAG	TCA	TAT	AAC	TTG	AAG	AGT	AAA	ATT	TGG	GCA	CCA	ACT	TCG	CAG	CCA	CCA	AAG	CAA	2035
622	Leu	Arg	Ile	Gln	Lys	Ser	Tyr	Asn	Leu	Lys	Ser	Lys	Ile	Trp	Ala	Pro	Thr	Ser	Gln	Pro	Pro	Lys	Gln	644
2036	CAG	CCC	CTC	ACA	TGG	TAT	AAG	GCA	GTA	GTA	GAT	GCG	CCT	CCT	GGT	AAT	GAA	CCT	GTT	GCA	CTT	GAT	ATG	2104
645	Gln	Pro	Leu	Thr	Trp	Tyr	Lys	Ala	Val	Val	Asp	Ala	Pro	Pro	Gly	Asn	Glu	Pro	Val	Ala	Leu	Asp	Met	667
2105	ATT	CAT	ATG	GGA	AAA	GGA	ATG	GCT	TGG	TTG	AAT	GGA	CAA	GAA	ATT	GGC	AGA	TAT	TGG	CCG	AGG	AGA	ACT	2173
668	Ile	His	Met	Gly	Lys	Gly	Met	Ala	Trp	Leu	Asn	Gly	Gln	Glu	Ile	Gly	Arg	Tyr	Trp	Pro	Arg	Arg	Thr	690
2174	TCT	AAA	TAT	GAG	AAT	TGT	GTT	ACT	CAA	TGT	GAC	TAC	AGA	GGC	AAA	TTT	AAC	CCT	GAT	AAG	TGT	GTC	ACT	2242
691	Ser	Lys	Tyr	Glu	Asn	Cys	Val	Thr	Gln	Cys	Asp	Tyr	Arg	Gly	Lys	Phe	Asn	Pro	Asp	Lys	Cys	Val	Thr	713
2243	GGC	TGT	GGA	CAA	CCT	ACA	CAG	AGA	TGG	TAT	CAT	GTG	CCA	CGA	TCT	TGG	TTC	AAG	CCA	TCA	GGA	AAT	GTC	2311
714	Gly	Cys	Gly	Gln	Pro	Thr	Gln	Arg	Trp	Tyr	His	Val	Pro	Arg	Ser	Trp	Phe	Lys	Pro	Ser	Gly	Asn	Val	736
2312	TTA	ATT	ATC	TTT	GAG	GAA	ATA	GGT	GGA	GAT	CCC	TCT	CAA	ATT</										

DNASIS  
Multiple Edit1Figure 3  
Sheet 1 of 4

		10	20	30	40	50	
TBG1-ORF	-24	.....	.....	MGFWMA	MLMLLLCLW	VSCGISVSYD	26
TBG2-ORF	-14	.....	MSRRKT	LNFPILITVL	TIHFVIVAGE	YFKPFNVTYD	36
TBG3-ORF	-20	.....	.....	MGCTLLMLN	VLLVLLGSWV	FSGTASVSYD	30
TBG4-ORF	-22	.....	.....	MLRTNVLL	LLVTCILDFE	SSVKASVSYD	28
TBG5-ORF	1	-----	-----	-----	-----	-----	50
TBG6-ORF	1	-----	-----	-----	-----	-----	50
TBG7-ORF	-1	..MNIMSCLS	NFKFVFLAST	VIWMIVMSSS	LAAVDASNVT	TIGTDSVTYD	49
apple	-21	.....	.....	..MGVGIOIMW	SILLFSCIF	SAASASVSYD	29
carnation	-16	.....	..MLCG	KENNVMMML	VYVFVITLI	SCVYGNWYD	34
asparagus	-20	.....	.....	MALFLVLM	VALLAAVWSP	PATIASVTYD	30
broccoli	-20	.....	.....	MMKQFNLLS	LFLLITISFG	SANSTIVSYD	30
Lupin	-12	.....	..MEGSRIVM	ESIMSRRNPH	MVLLILFFWV	CYVNASVTYD	38
		60	70	80	90	100	
TBG1-ORF	27	HKALIVNGOR	KILLSSSTHY	RRSTPEMWD	LIOKAKEGGV	IVTQTAAYN	76
TBG2-ORF	37	NRALFEGKR	RMHSAGHY	BRADPEMWT	LIARSKEGGA	IVTQTAAYN	86
TBG3-ORF	31	HRALIVNGOR	KILLSSSVHY	RRSTPEMWD	LIOKAKEGGV	IVTQTAAYN	80
TBG4-ORF	29	DRALFEGKR	KILLSSSTHY	RRSTPEMWD	LIOKAKEGGV	IVTQTAAYN	78
TBG5-ORF	51	-----	-----	-----	-----	-----	100
TBG6-ORF	51	-----	-----	-----	-----	-----	100
TBG7-ORF	50	RRSLFEGOR	KLEICAGHY	RRSTPEMWD	LIOKAKEGGV	IVTQTAAYN	99
apple	30	HKALFEGOR	KILLSSSTHY	RRSTPEMWD	LIOKAKEGGV	IVTQTAAYN	79
carnation	35	YRAKINDOR	RMHSAGHY	BRADPEMWT	LIARSKEGGA	IVTQTAAYN	84
asparagus	31	HKSLFEGOR	KILLSSSTHY	RRSTPEMWD	LIOKAKEGGV	IVTQTAAYN	80
broccoli	31	ERKSLFEGOR	KILLSSSTHY	RRSTPEMWD	LIOKAKEGGV	IVTQTAAYN	80
Lupin	39	HKALFEGOR	KILLSSSTHY	RRSTPEMWD	LIOKAKEGGV	IVTQTAAYN	88
		110	120	130	140	150	
TBG1-ORF	77	GHEPSEGKYV	REERYDAV	RVVCEAGYV	VHLRIGGAG	AEWNSGGFV	126
TBG2-ORF	87	GHEPSEGKYV	REERYDAV	RVVCEAGYV	VHLRIGGAG	AEWNSGGFV	136
TBG3-ORF	81	GHEPSEGKYV	REERYDAV	RVVCEAGYV	VHLRIGGAG	AEWNSGGFV	130
TBG4-ORF	79	GHEPSEGKYV	REERYDAV	RVVCEAGYV	VHLRIGGAG	AEWNSGGFV	128
TBG5-ORF	101	LHSEVRNOYD	REERYDAV	RVVCEAGYV	VHLRIGGAG	AEWNSGGFV	150
TBG6-ORF	101	VHSEVRNOYD	REERYDAV	RVVCEAGYV	VHLRIGGAG	AEWNSGGFV	150
TBG7-ORF	100	GHEPSEGKYV	REERYDAV	RVVCEAGYV	VHLRIGGAG	AEWNSGGFV	149
apple	80	GHEPSEGKYV	REERYDAV	RVVCEAGYV	VHLRIGGAG	AEWNSGGFV	129
carnation	85	GHEPSEGKYV	REERYDAV	RVVCEAGYV	VHLRIGGAG	AEWNSGGFV	134
asparagus	81	GHEPSEGKYV	REERYDAV	RVVCEAGYV	VHLRIGGAG	AEWNSGGFV	130
broccoli	81	AHEPSEGKYV	REERYDAV	RVVCEAGYV	VHLRIGGAG	AEWNSGGFV	130
Lupin	89	GHEPSEGKYV	REERYDAV	RVVCEAGYV	VHLRIGGAG	AEWNSGGFV	138
		160	170	180	190	200	
TBG1-ORF	127	WLKAVPGISF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	KLYETQGGPI	176
TBG2-ORF	137	WLKAVPGIET	RTDNEPFKAA	MOKETKIVD	MMK-----AE	KLYETQGGPI	186
TBG3-ORF	131	WLKAVPGISF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	KLYETQGGPI	180
TBG4-ORF	129	WLKAVPGMEF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	KLYETQGGPI	178
TBG5-ORF	151	WLHFIPIGIEF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	KLYETQGGPI	200
TBG6-ORF	151	WLKAVPGISF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	KLYETQGGPI	200
TBG7-ORF	150	WLHVPGETTF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	KLYETQGGPI	199
apple	130	WLKAVPGIET	RTDNEPFKAA	MOKETKIVD	MMK-----AE	KLYETQGGPI	179
carnation	135	WLKAVPGIET	RTDNEPFKAA	MOKETKIVD	MMK-----AE	KLYETQGGPI	184
asparagus	131	WLKAVPGIET	RTDNEPFKAA	MOKETKIVD	MMK-----AE	KLYETQGGPI	180
broccoli	131	WLHNPDMKF	RTDNEPFKAA	MOKETKIVD	MMK-----AE	KLYETQGGPI	180
Lupin	139	WLKAVPGIET	RTDNEPFKAA	MOKETKIVD	MMK-----AE	KLYETQGGPI	188
		210	220	230	240	250	
TBG1-ORF	177	ILSQ-IENEF	GP--MEWELG	EPGRVYSEWA	AKMAVDLGTG	VPWIMCKQD-	226
TBG2-ORF	187	ILSQ-IENEF	GN--VESSFG	PKGKLYMKWA	AEMAVGLGAG	VPWIMCKQD-	236
TBG3-ORF	181	ILSQ-IENEF	GP--MEWELG	APGKSYAQA	AKMAVGLDTG	VPWIMCKQD-	230
TBG4-ORF	179	IMAQ-IENEF	GP--VEWEIG	APGKAYTKWA	AQMAVGLKTG	VPWIMCKQD-	228
TBG5-ORF	201	ILSQ-IENEF	GNGDIESRYG	PRAKPYVNW	ASMATSLNTG	VPWIMCKQD-	250
TBG6-ORF	201	RMSMGLKPRY	----LEHRDI	SIQHGLQIWQ	----LDLNTG	VPWIMCKQD-	250
TBG7-ORF	200	ILSQ-VENEY	G--YYENAYG	EGGKRYALWA	AKMALSONTG	VPWIMCKQD-	249
apple	180	ILSQ-IENEF	GP--VEWEIG	APGKAYTKWA	AQMAVGLDTG	VPWIMCKQD-	229
carnation	185	ILNQ-IENEF	GP--VEWEIG	APGKAYTHWA	AQMAQSLNAG	VPWIMCKQD-	234

DNASIS  
Multiple edit1Figure 3  
Sh et 2 f 4

asparagus	181	TCSC--TENEY	GP--VEYVDG	AAGKSYKINWA	ACGAYGNNNG	GVAVMCKOB-	230
broccoli	181	TCAC--TENEY	GN--VISSYG	AEGKAYIDAC	ANMANSBDIG	GVAVMCKOB-	230
Lupin	189	TCSC--TENEY	GP--VEWEIG	APGKAYTOWA	ACGAYVSDIG	GVAVMCKOB-	238
		260	270	280	290	300	
TBG1-ORF	227	DVDPDIINTC	NGFYCDYFTP	NKANKPKIWT	EAWTAWETIC	GVAVMCKOB-	276
TBG2-ORF	237	DAPEYIIDTC	NAYYCDGFTP	NSEKKPKIWT	ENWNGWFADW	GERLPYRPESE	286
TBG3-ORF	231	DAPDPIINAC	NGFYCDYFSP	NKAYKPKIWT	EAWTAWETIC	GVAVMCKOB-	280
TBG4-ORF	229	DAPDPVIDTC	NGFYCDGFRP	NKRYKPKIWT	EAWTAWETIC	GVAVMCKOB-	278
TBG5-ORF	251	DAPPSVINTC	NGFYCDQPKQ	NSDKTPKMT	EAWTAWETIC	GVAVMCKOB-	300
TBG6-ORF	251	DAPDPVINTC	NGFYCDNFFP	NKPKPKIWT	EAWSGWFSEI	GVAVMCKOB-	300
TBG7-ORF	250	DAPDPVIDTC	NSFYCDQFKP	ISHPKPKIWT	ENWPGWETIC	GVAVMCKOB-	299
apple	230	DAPDPVIDTC	NGFYCDNFKP	NKDYKPKIWT	EAWTAWETIC	GVAVMCKOB-	279
carnation	235	DVDPDIINTC	NGFYCDGFPV	KDKSKPKIWT	ENWPGWETIC	GVAVMCKOB-	284
asparagus	231	DAPDPVINTC	NGFYCDYFSP	NKINKPKIWT	EAWTAWETIC	GVAVMCKOB-	280
broccoli	231	HADPMIETC	NGFYCDQYKP	SNSSPKIWT	EAWTAWETIC	GVAVMCKOB-	280
Lupin	239	DAPDPIINTC	NGFYCDNFTP	NKINKPKIWT	EAWTAWETIC	GVAVMCKOB-	288
		310	320	330	340	350	
TBG1-ORF	277	DMFAVAREFF	OTGGSSEINNY	MYHGGTNEGR	TSCEPMAI	GVAVMCKOB-	326
TBG2-ORF	287	DMFAVAREFF	ORGGSSEINNY	MYHGGTNEGR	TSCEPMAI	GVAVMCKOB-	336
TBG3-ORF	281	DMFAVAREFF	ORGGSSEINNY	MYHGGTNEGR	TSCEPMAI	GVAVMCKOB-	330
TBG4-ORF	279	DMFAVAREFF	ORGGSSEINNY	MYHGGTNEGR	TSCEPMAI	GVAVMCKOB-	328
TBG5-ORF	301	DMFAVAREFF	ORGGSSEINNY	MYHGGTNEGR	TSCEPMAI	GVAVMCKOB-	350
TBG6-ORF	301	DMFAVAREFF	ORGGSSEINNY	MYHGGTNEGR	TSCEPMAI	GVAVMCKOB-	350
TBG7-ORF	300	DMFAVAREFF	ORGGSSEINNY	MYHGGTNEGR	TSCEPMAI	GVAVMCKOB-	349
apple	280	DMFAVAREFF	ORGGSSEINNY	MYHGGTNEGR	TSCEPMAI	GVAVMCKOB-	329
carnation	285	DMFAVAREFF	ORGGSSEINNY	MYHGGTNEGR	TSCEPMAI	GVAVMCKOB-	334
asparagus	281	DMFAVAREFF	ORGGSSEINNY	MYHGGTNEGR	TSCEPMAI	GVAVMCKOB-	330
broccoli	281	DMFAVAREFF	ORGGSSEINNY	MYHGGTNEGR	TSCEPMAI	GVAVMCKOB-	330
Lupin	289	DMFAVAREFF	ORGGSSEINNY	MYHGGTNEGR	TSCEPMAI	GVAVMCKOB-	338
		360	370	380	390	400	
TBG1-ORF	327	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PTVSWPGKOL	GVAVMCKOB-	376
TBG2-ORF	337	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PTVSWPGKOL	GVAVMCKOB-	386
TBG3-ORF	331	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PTVSWPGKOL	GVAVMCKOB-	380
TBG4-ORF	329	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PTVSWPGKOL	GVAVMCKOB-	378
TBG5-ORF	351	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PTVSWPGKOL	GVAVMCKOB-	400
TBG6-ORF	351	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PTVSWPGKOL	GVAVMCKOB-	400
TBG7-ORF	350	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PTVSWPGKOL	GVAVMCKOB-	399
apple	330	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PTVSWPGKOL	GVAVMCKOB-	379
carnation	335	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PTVSWPGKOL	GVAVMCKOB-	384
asparagus	331	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PTVSWPGKOL	GVAVMCKOB-	380
broccoli	331	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PTVSWPGKOL	GVAVMCKOB-	380
Lupin	339	GLRROPKWH	LKDLHRAIKL	CEPALVSD	PTVSWPGKOL	GVAVMCKOB-	388
		410	420	430	440	450	
TBG1-ORF	377	-----	GACAAFLANY	NQHSFAKVA	GNMHNLPW	SISILPDCKN	426
TBG2-ORF	387	NIGQYMSLNE	GICAAFIANI	DEHESATVKF	YGQFTLPPW	SVVF---CQI	436
TBG3-ORF	381	-----	GSCAAFLANY	DQHSFATVSF	ANRHNLPW	SISILPDCKN	430
TBG4-ORF	379	-----	GACAAFLSNY	DSRYSVKVTF	QNRPNLPW	SISILPDCKT	428
TBG5-ORF	401	-----	-----	-----	-----	-----	450
TBG6-ORF	401	-----	-----	-----	-----	-----	450
TBG7-ORF	400	-----	GACAAFLANM	DDKNDKVQF	RHVSYHLPW	SVSILPDCKN	449
apple	380	-----	D-CAAFANY	DAKYSVKVSF	GGQYDLPPW	SISILPDCKT	429
carnation	385	-----	GSCAAFLANY	DPKWSVKVTF	SGMEFELPAW	SISILPDCKK	434
asparagus	381	-----	-SCAAFLANF	NSRYATVTF	NGMHNLPW	SVSILPDCKT	430
broccoli	381	S-----	-SC--FIGNV	NATADALVNF	KGKDYNPW	SVSILPDCKT	430
Lupin	389	-----	A-CAAFANY	NTDYSTQVKF	GNGQYDLPPW	SISILPDCKT	438
		460	470	480	490	500	
TBG1-ORF	427	TVYNTARVGA	QSAQM--K--	-----	MTP	VSRGFS--WE	476
TBG2-ORF	437	AEIQQLSTQLR	WGHLQSKQW	AQILFQLGII	LCFYKLSLKA	SSESFSQSWM	486
TBG3-ORF	431	TVFNTARIGA	QSAQM--K--	-----	MTP	VSRGLP--WQ	480
TBG4-ORF	429	AVYNTAQVNS	QSSSI--K--	-----	MTP	AGGGLS--WQ	478
TBG5-ORF	451	-----	-----	-----	-----	-----	500

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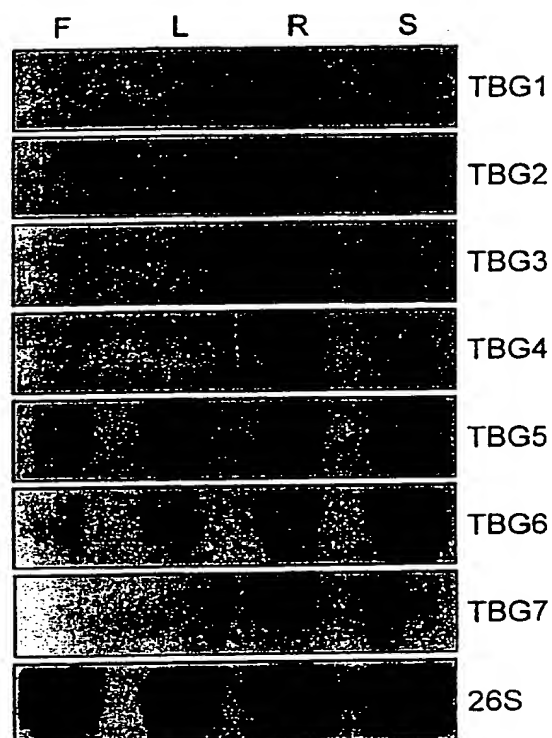
Figure 3  
She 13 of 4

TBG6-ORF	451	VAFNTAKVGC	OTSIVNMAP	ED	HPTASSE	KRDIKSLONE	499
TBG7-ORF	450	EYVNTAKVGS	OSSQV-Q		MTP	VHSGEP	479
apple	430	EYVNTAKVNE	PSPKLHSE		MTP	VI SNLN	484
carnation	435	TUFTIARVGA	OTTTM-E		MOY	LG-GEE	480
asparagus	431	EAVNTARVNT	QTSIIITDS	-C-	D	EPEKLRWTR	480
broccoli	431	EVFNIAKVNS	PRLHR-K		MTP	VNSAFA-WO	488
Lupin	439						
		510	520	530	540	550	
TBG1-ORF	477	S-FNEEAASH	EDD-TSIVVC	MSDOINTTRE	VSDYLWMTD	IELDPTE-CF	526
TBG2-ORF	487	T-LKEPLGWV	GDKN-EISKG	TDPHLNVTKG	QSDXWYLTR	TYLSDDDISF	536
TBG3-ORF	481	S-FNEETSSY	EDS-SFTVVG	LEDOINTTRE	VSDYLWYSTD	VKIDSRK-KF	530
TBG4-ORF	479	S-YNEEPTPA	DDSDILTAG	EWOKNVURE	SSDXLWYMIN	VNTASNE-CF	528
TBG5-ORF	501						550
TBG6-ORF	501						550
TBG7-ORF	500	V-FKETAGVW	GVADEKNG	FVDHENTKGB	STPDMWTTS	IFVHAEE-DE	549
apple	480	S-ETERTSS	BETIRJLDG	LYBOLHIURE	TTHELYMTTH	ITIGSDI-AF	529
carnation	485	S-YSDEVPTA	DSPGTREKK	LYBOLMIWP	KSGWLWMTD	AWLDGNB-CF	534
asparagus	481	A-YTEDIDAL	NEN-RTKYDG	IVPOLSTABE	RSPHASTATY	VHLIAKNE-EE	530
broccoli	481	PEFTTOKTIL	KGSGDLIARG	IVDCKOVINE	ASBLHAYTHR	VHLDKKOPIW	530
Lupin	489	S-YNEEPASS	SENDPVGYA	WEZVGVERD	SSDXLWYLTG	VNTGPND---	538
		560	570	580	590	600	
TBG1-ORF	527	LNSGN-WPWV	TVFSAGHATH	VEONCOGISA	VVSSENBRGI	TESNGTNMBA	576
TBG2-ORF	537	WEENDVSEFI	DIDSMDRFVR	IKWACOPASS	VKGGW---I	KVQVPVLSVO	586
TBG3-ORF	531	LRGCK-WPWV	TIMSAGHATH	VEANCOGAGR	AVGSLKPKKI	TFSKAVLLRA	580
TBG4-ORF	529	LKNCK-DPYV	TVMSAGHVH	VEANKESGR	VYGTLENPKI	TYSGNVKLEA	578
TBG5-ORF	551						600
TBG6-ORF	551						600
TBG7-ORF	550	LRN-RGTAMV	FVESKSHMH	VEINCKHOAS	ASENGTVPOF	KEGTPIAAKA	599
apple	530	LKNCK-SLP	TLFSAGHAIN	VEINCOLSFI	VVSLENBRKI	SRSNNMLBS	579
carnation	535	LKCKD-EPMV	TVMSAGHVH	VEANCOLOH	VKSIAKOPH	USOKVMATA	584
asparagus	531	LKTCK-YPYV	TVMSAGHVH	VEINCOLSFI	AVESLDRPKI	BYSGSAKILWA	580
broccoli	531	SRNMS---	RVHSNAHVH	AVANKGVVN	QIVRNKFDF	REEKKVNLVH	580
Lupin	539	IKDCK-WPWV	TAMSAGHAIN	VEINCOVAGA	AVESLDRRI	TESOSVNLV	588
		610	620	630	640	650	
TBG1-ORF	577	GVNKISLSLI	AVGLEPNVGH	FEYNAGVLG	FWSENGNENG	P---RDLTWO	626
TBG2-ORF	587	GYNDILILSE	TVGLONYGAF	LEKDGAFFKG	QIKLITCKSC	D---INLTITS	636
TBG3-ORF	581	GVNKISLSLI	AVGLEPNVGF	FEYNAGVLG	FWSLIGLDBG	K---RDLTWO	630
TBG4-ORF	579	GINKISLSLV	SVGLEPNVGH	YDTWNAVILG	PVTLISGLNEG	S---RNLAKQ	628
TBG5-ORF	601						650
TBG6-ORF	601						650
TBG7-ORF	600	GKNEISLSLM	TVGLQTAGAF	YE-WIGAGPT	SVKVAGFKTG	T---MDLTAS	649
apple	580	GINKLALLSI	SVGLEPNVGH	FEYNAGVLG	ETIKGLNSG	T---WDMSGW	629
carnation	585	GVNRISLSLA	SVGLANVGVH	FERYNQGVLG	PVTLISGLNEG	T---RDLTWO	634
asparagus	581	GSNKISLSLV	SVGLEPNVGH	FEYNAGVLG	PVTLISGLNEG	K---RDLSLQ	630
broccoli	581	GTNHLALLSV	SVGLONYGPF	FESGPTGNG	EUKLVGYKGD	ETIEKDLSEKH	630
Lupin	589	GVNKISLSLV	SVGLANVGVH	FEYNAGVLG	PVTLISGLSSG	T---WDSLKQ	638
		660	670	680	690	700	
TBG1-ORF	627	KWFYKVLKLG	EALSLSLSLG	SPSVE--WVE	GSLVAQKQPL	SWYKTTFNAP	676
TBG2-ORF	637	LWTYQVGLRG	EFLEVYDVNS	TESAG--WTE	FPTGITPSVF	SWYKIKFDAP	686
TBG3-ORF	631	KWSYKVLKLG	EALSLSLSLG	SSSVE--WVE	GSLVAQRQPL	TWYKSTFNAP	680
TBG4-ORF	629	KWSYKVLKLG	ESLSLSLSLG	SSSVE--WVR	GSLMAQKQPL	TWYKATFNAP	678
TBG5-ORF	651						700
TBG6-ORF	651						700
TBG7-ORF	650	AWTYKIGLOG	EHLRIQSYN	LKSKI--WAP	TSOPPQQOPL	TWYKAVVDAP	699
apple	630	KWTYKTGLKG	EALGLHTVTG	SSSVE--WVE	GPSMAEQOPL	TWYKATFNAP	679
carnation	635	YWSYKIGTKG	EBQOVYNSGG	SSHVQ--WGP	PAW---KOPL	VWYKTTFDAP	684
asparagus	631	KWTYQIGLHG	ETLSLSLSLTG	SNSVE--WGE	AS---QKQPL	TWYKTTFNAP	680
broccoli	631	QWDYKIGLNG	FNHKLFSMKS	AGHHHRKWF	EKLPAQRM-L	SWYKANFKAP	680
Lupin	639	KWSYKIGLKG	ESLSLSLHTEAG	SNSVE--WVQ	GSLVAKKQPL	AWYKTTFNAP	688
		710	720	730	740	750	
TBG1-ORF	677	DGNEPLALDM	NTMGKGQVWI	NGQSLGRHWP	AYKSS-GSCS	V-CNYTGWFD	726

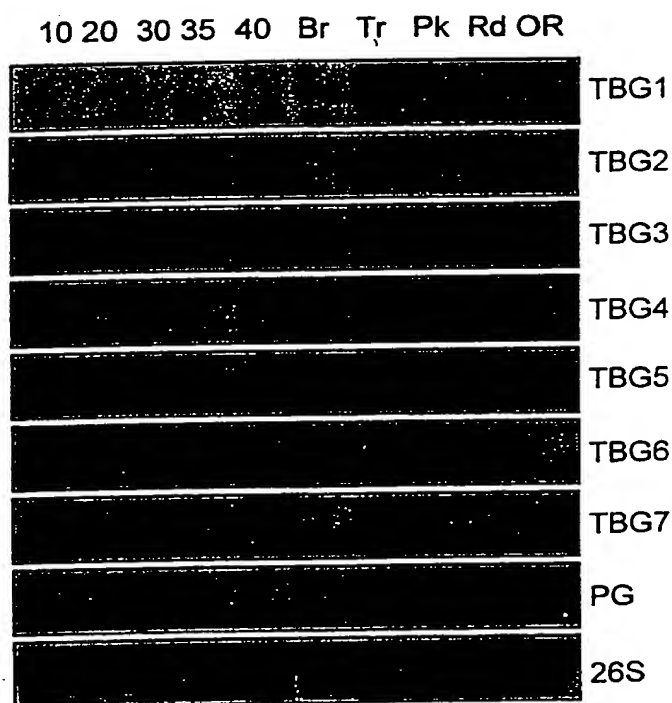


DNASIS  
Multiple Edit1Figure 3  
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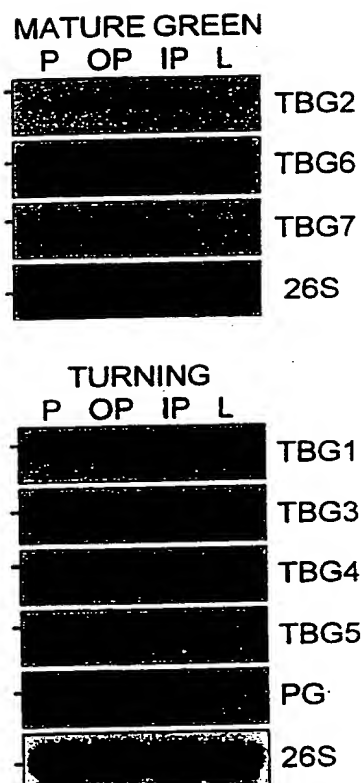
TBG2-ORF	687	GCTDPVALDF	SSMGKGOAW	NHHVGRWWT	LVAPN-NGGG	RTGDIRGAPH	736
TBG3-ORF	681	AGNDPLALL	NTMGKGOVWT	NGSLGRWWP	GYKAS-GNEG	A-CNYAGWPN	730
TBG4-ORF	679	GGNDPLALL	ASMGKGOIWT	NSEGVRHWP	GHTAQ-GDCS	K-CSYAGTFN	728
TBG5-ORF	701	-----	-----	-----	-----	-----	750
TBG6-ORF	701	-----	-----	-----	-----	-----	750
TBG7-ORF	700	PGNEFVALIM	IHMKGMAWL	NGOEIGRYWP	RRTSKYENCV	TQCDIRGKFN	749
apple	680	PGDAPLALL	GSMGKGOIWT	NGOSVGRHWP	GYIAR-GSGG	D-CSYAGTYD	729
carnation	685	GGNDPLALL	GSMGKGOAWT	NGOSIGRHWS	NNIAK-GSCN	INCNYAGTYT	734
asparagus	681	PGNEFVALIM	NTMGKGOIWT	NGOSIGRYWP	AYKAS-GSGG	S-CDYRGTYN	730
broccoli	681	LKCDPVTIVL	NGLKGEVWV	NGOSIGRYWP	SFNSSDGEGT	EECDYRGEYG	730
Lupin	689	AGNDPLALL	GSMGKGEVWV	NGOSIGRHWP	GNKAR-GNEG	N-CNYAGTYT	738
TBG1-ORF	727	KKKCLTINCE	GSORWYHVP	SMYPTGNLL	V-VFEENGGD	PYGITLVKRE	776
TBG2-ORF	737	SDKCRTHCGE	ITQAWYHIP	SMYKTLANVL	V-IFFEETDKT	PFDSISTRS	786
TBG3-ORF	731	KKKCLSNCE	ASORWYHVP	SMYPTGNLL	V-LFEENGGG	PHGSLVKRE	780
TBG4-ORF	729	KKKCOIVCGO	ESORWYHVP	SMYKPSGILL	V-VFEENGGN	ETGSLVKRS	778
TBG5-ORF	751	-----	-----	-----	-----	-----	800
TBG6-ORF	751	-----	-----	-----	-----	-----	800
TBG7-ORF	750	PDKCVTHCGO	PTORWYHVP	SMYKPSGIVL	I-IFFEETDKT	ESORFVSMK	799
apple	730	DKKCRTHCGE	ESORWYHIP	SMYKPSGIVL	V-VFEENGGD	ESORFVSMK	779
carnation	735	ETKCLSDGCK	SSORWYHVP	SMYKPSGIVL	V-VFEENGGD	TKWVSLVKRT	784
asparagus	731	KKKCLSNCE	ASORWYHVP	SMYKPSGIVL	V-VFEENGGD	ETGSLVKRS	780
broccoli	731	SDKCAFMECK	PTORWYHVP	SMYKPSGIVL	V-VFEENGGD	ESORFVSMK	780
Lupin	739	DTKCLANCGO	ESORWYHVP	SMYKPSGIVL	V-VFEENGGD	ETGSLVKRS	788
TBG1-ORF	777	IGSVCAEVEE	KG-POLLNMG	RLVSKFDRK	LR-PRKHLK	GAPGOKISSA	826
TBG2-ORF	787	TETICAOVSE	KHYEPHKKWS	HSEFDRKLSL	MDKTPEMHIO	QDEGHTESST	836
TBG3-ORF	781	VASVCADINE	KG-POLLNMG	MOASKVDKRF	LR-PRKHLK	GAPGOKISSA	830
TBG4-ORF	779	-----	-----	-----	-----	-----	828
TBG5-ORF	801	-----	-----	-----	-----	-----	850
TBG6-ORF	801	-----	-----	-----	-----	-----	850
TBG7-ORF	800	VSGACGHLV	-DHESFD-V	ENLQSEIEN	DKNRPTLSLK	CPTNINTESSV	849
apple	780	IR-	-----	-----	TA	ND-AK	829
carnation	785	IR-	-----	-----	-----	-----	834
asparagus	781	VASVCADVEE	LQ-PIMINAR	TKBYG	-R-PRVHLS	QDEGOKMSKI	830
broccoli	781	TGRVCAKAHE	-----	-----	-----	-----	830
Lupin	789	-----	-----	-----	-----	-----	838
TBG1-ORF	827	KFASFGTPEG	VCGNFOGSGC	HAPRSYDAFK	K-----NCVG	KESCSVQVTP	876
TBG2-ORF	837	EFASYGSPNG	SOOKESOGKC	HAANLSV--	---VSQACIG	RTSCSIGISN	886
TBG3-ORF	831	KFASFGTPOG	VCGSFREGSC	HAFHSYDAFE	R-----YCIG	QNSCSVPVTP	880
TBG4-ORF	829	-----	-----	-----	-----	-----	878
TBG5-ORF	851	-----	-----	-----	-----	-----	900
TBG6-ORF	851	-----	-----	-----	-----	-----	900
TBG7-ORF	850	KFASFGNPNG	TCGSYMLGDC	HDQNSAALVE	K-----VCLN	QNECALEMSS	899
apple	830	-----	-----	-----	-----	-----	879
carnation	835	-----	-----	-----	-----	-----	884
asparagus	831	KFASFGTPOG	TCGSFSEGSC	HAHKSYDAFE	QEGLMQNCVG	QEFCSVNAP	880
broccoli	831	KFASFGNPSG	QCGSFAAGSC	EGAKDAVKV-	---VAKECVG	KLNCNMVSS	880
Lupin	839	-----	-----	-----	-----	-----	888
TBG1-ORF	877	ENFGGDP-CR	NVLKKLSVEA	IGS-----	-----	-----	926
TBG2-ORF	887	GVFG-DP-CR	HVVKSLAVQA	KCSPPPDIST	SASS-----	-----	936
TBG3-ORF	881	EIFGGDP-CP	HVMKKLSVEV	IGS-----	-----	-----	930
TBG4-ORF	879	-----	-----	-----	-----	-----	928
TBG5-ORF	901	-----	-----	-----	-----	-----	950
TBG6-ORF	901	-----	-----	-----	-----	-----	950
TBG7-ORF	900	ANFNMQL-CP	STVKKLAVEV	NCS-----	-----	-----	949
apple	880	-----	-----	-----	-----	-----	929
carnation	885	-----	-----	-----	-----	-----	934
asparagus	881	EVFGGDP-CP	GTMKKLAVEA	ICE-----	-----	-----	930
broccoli	881	HKFGSNLDCC	DSPKRLFVEV	EC-----	-----	-----	930



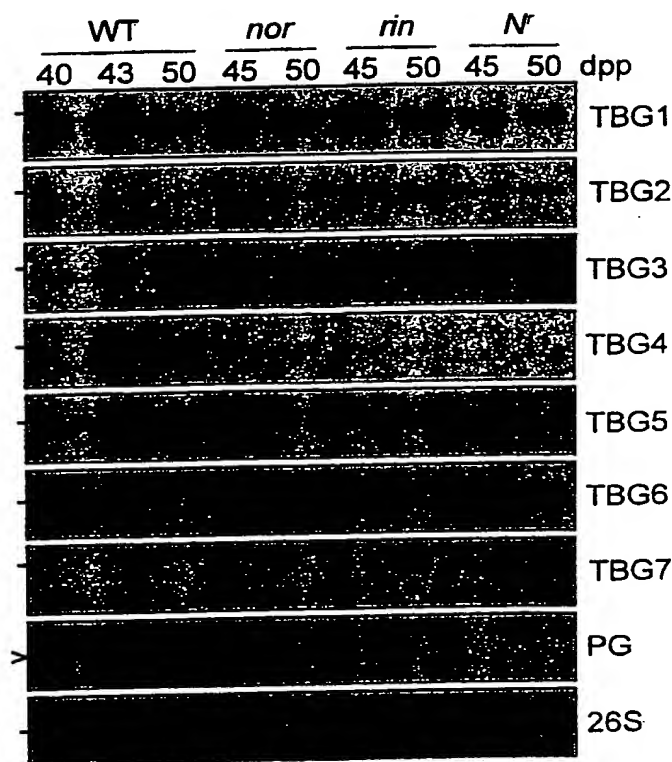
**Figure 4. Autoradiograph of northern blot analysis of TBG expression in various plant tissues.** Twenty  $\mu$ g of total RNA extracted from flowers (F), leaves (L), roots (R) and stems (S) was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown.



**Figure 5. Autoradiograph of northern blot analysis of TBG expression in fruit tissues.** Twenty  $\mu$ g of total RNA extracted from peel and outer pericarp tissue was loaded in each lane. Fruit were harvested at 10, 20, 30, 35, and 40 days post-pollination and at the breaker (Br), turning (Tr), pink (Pk), red (Rd) and over ripe (OR) stages. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. A cDNA clone for tomato polygalacturonase (PG) was also used as a probe to show a well characterized, fruit-ripening-specific control.



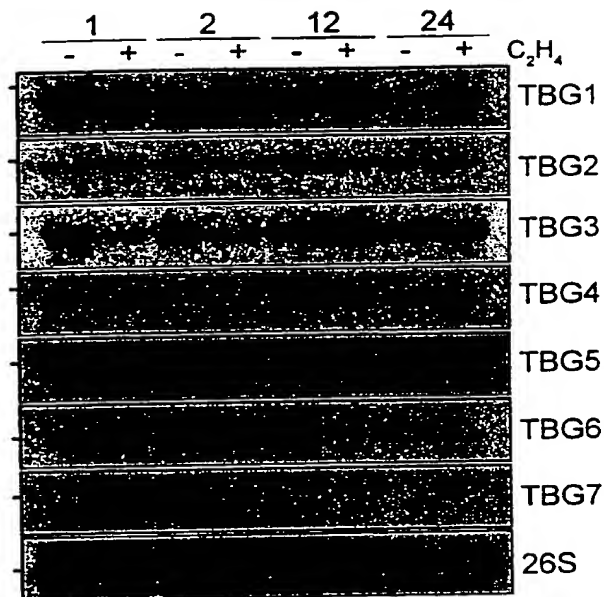
**Figure 6. Autoradiograph of northern blot analysis of TBG expression in fruit tissues.** Twenty  $\mu$ g of total RNA extracted from mature green or turning stage fruit peel (P), outer pericarp (OP), inner pericarp (IP) and locular (L) tissue was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. A cDNA clone for tomato polygalacturonase (PG) was also used as a probe to show a well characterized, fruit-ripening-specific control.



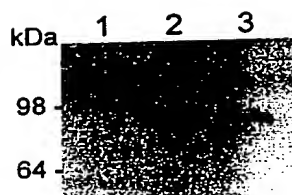
**Figure 7. Autoradiograph of northern blot analysis of TBG expression in normal and mutant fruit tissues.** Twenty  $\mu$ g of total RNA extracted from peel and outer pericarp tissue at various days post-pollination (dpp) was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. A cDNA clone for tomato polygalacturonase (PG) was also used as a probe to show a well characterized, fruit-ripening-specific control. The - and > marks on the left indicate the position of the tomato 27S and 18S rRNAs respectively.

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**Figure 8. Autoradiograph of northern blot analysis of TBG expression in response to ethylene treatment of mature green fruit tissues.** Twenty  $\mu\text{g}$  of total RNA extracted from peel and outer pericarp tissue at various times (1, 2, 12 and 24 hours) after treatment with (+) or without (-) 10 ppm ethylene was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control for each blot and one example is shown. The - marks on the left indicate the position of the tomato 27S rRNA.



**Figure 9. Western blot analysis of TBG4 expression by yeast.** A yeast clone was isolated that secreted high levels of FLAG-TBG4 fusion protein into the culture medium. Protein samples were separated in an 8% acrylamide gel, transferred to nitrocellulose and were blotted with M1 anti-FLAG primary antibody. Blots were washed and blotted with an alkaline-phosphatase conjugated secondary antibody and alkaline phosphatase activity was detected using Sigma Fast substrate. Lane 1, culture medium of an untransformed yeast clone was used as a negative control. Lane 2, culture medium of yeast clone expressing FLAG-TBG4 fusion protein. Lane 3, Affinity purified FLAG-TBG4 fusion protein.

Figure 10

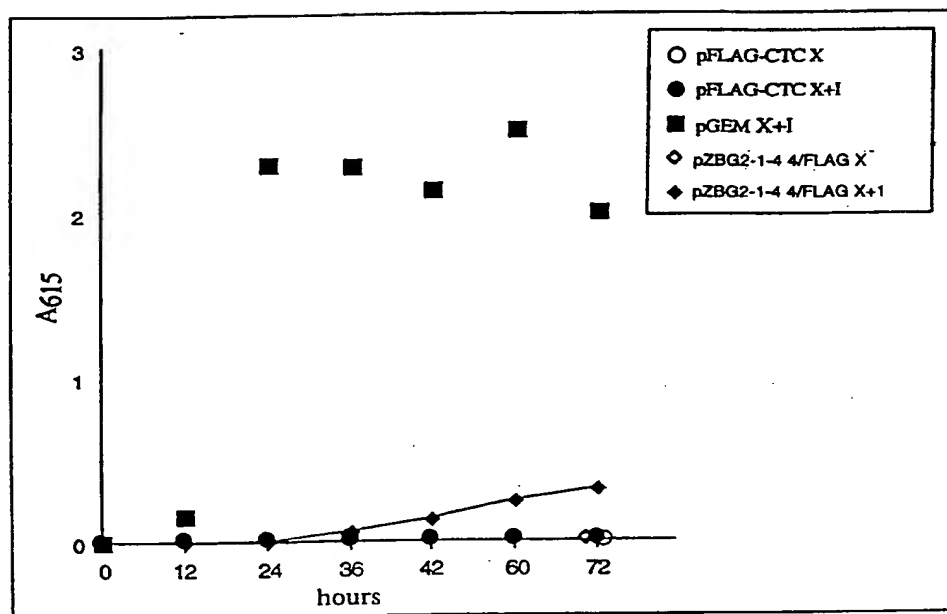
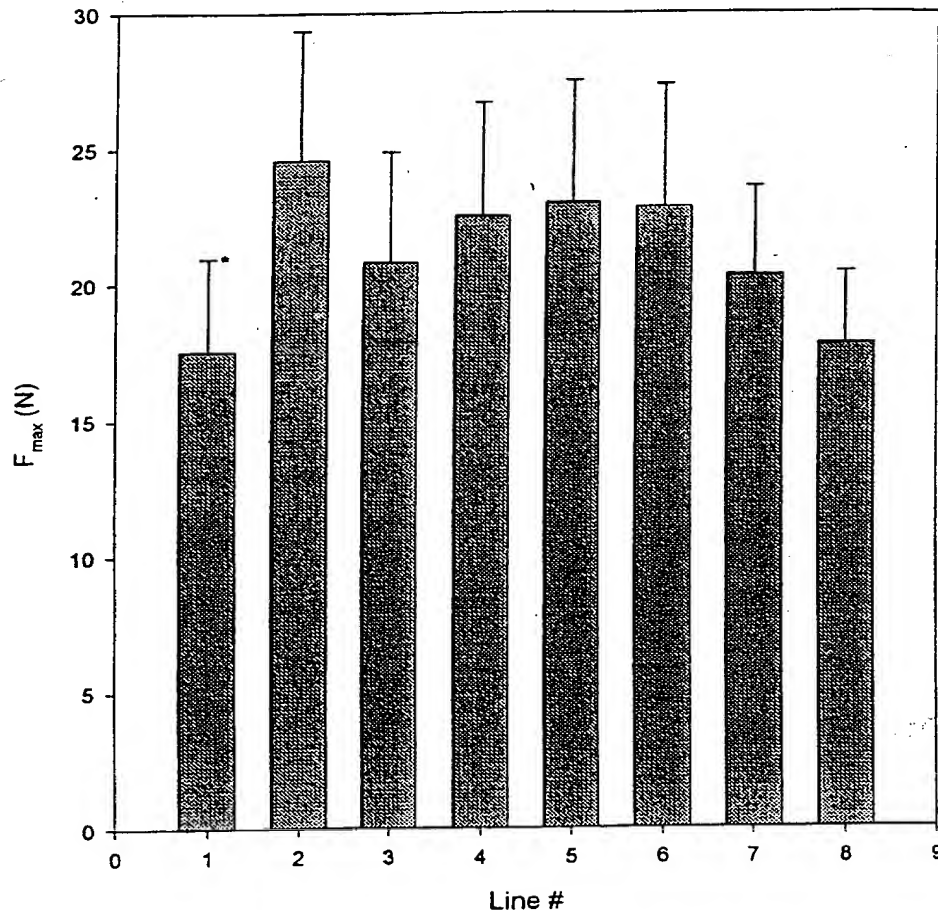




Figure 11A

Flat plate compression to 3 mm  
Breaker + 7 d



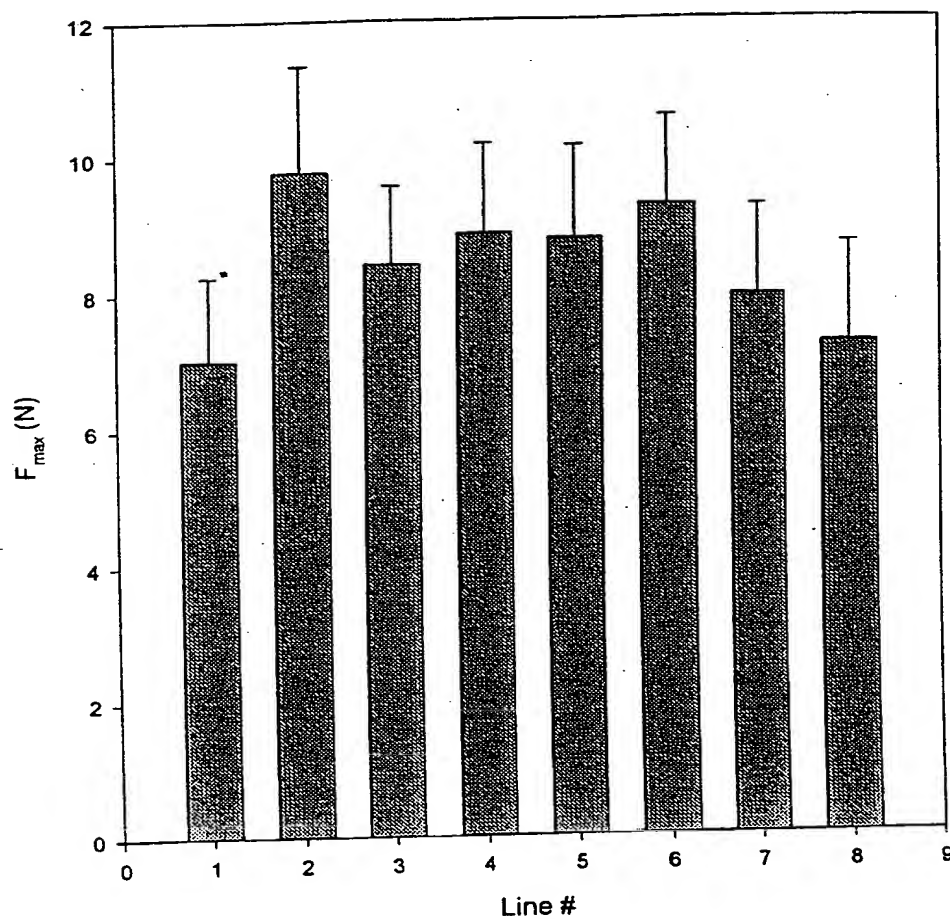
\* Standard Deviation

FP07 Line # FP07 mean FP07 std dev

1	17.52665	3.418542
2	24.56026	4.786548
3	20.81681	4.066194
4	22.54655	4.15923
5	23.03255	4.493091
6	22.84338	4.517462
7	20.36124	3.24608
8	17.81924	2.665468

Figure 11B

Spherical indenter to 3 mm  
Breaker + 7 d

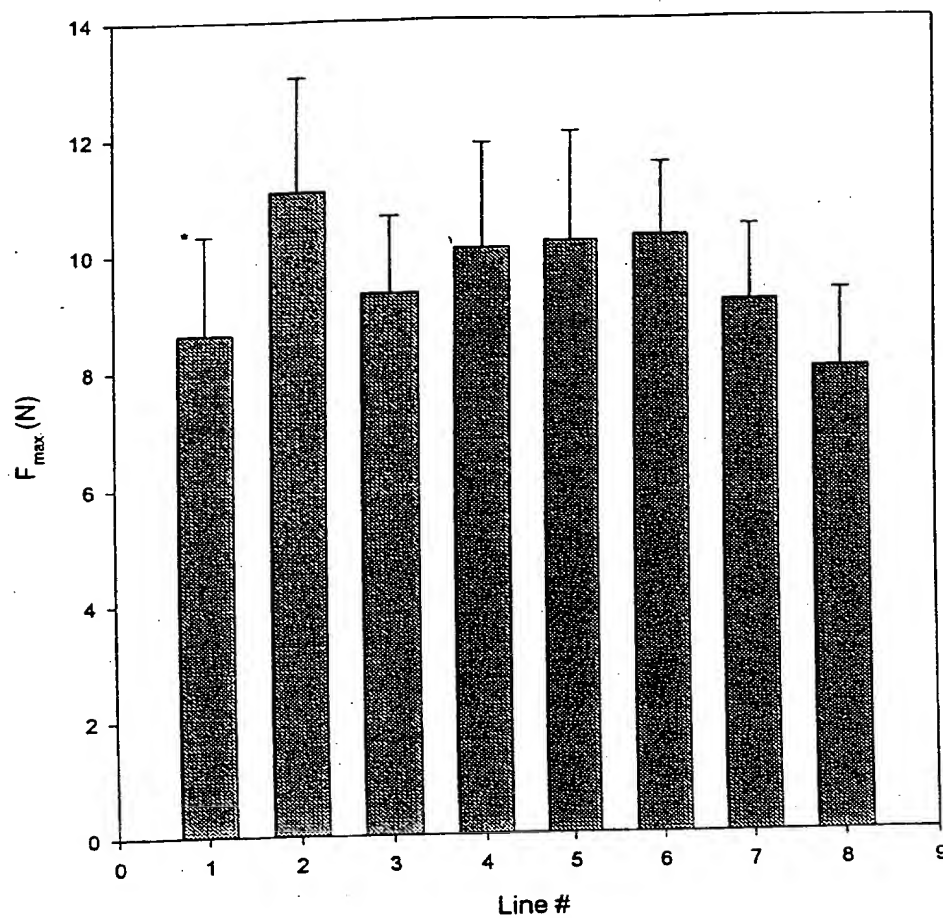


\* Standard Deviation

SP07 Line #	SP07 Mean	SP07 Std Dev
1	7.02	1.22
5	9.77	1.57
6	8.43	1.15
7	8.87	1.32
8	8.78	1.36
9	9.28	1.29
11	7.96	1.30
12	7.26	1.45

Figure 11C

4-mm cylindrical indenter to 1 mm  
Breaker + 7 d

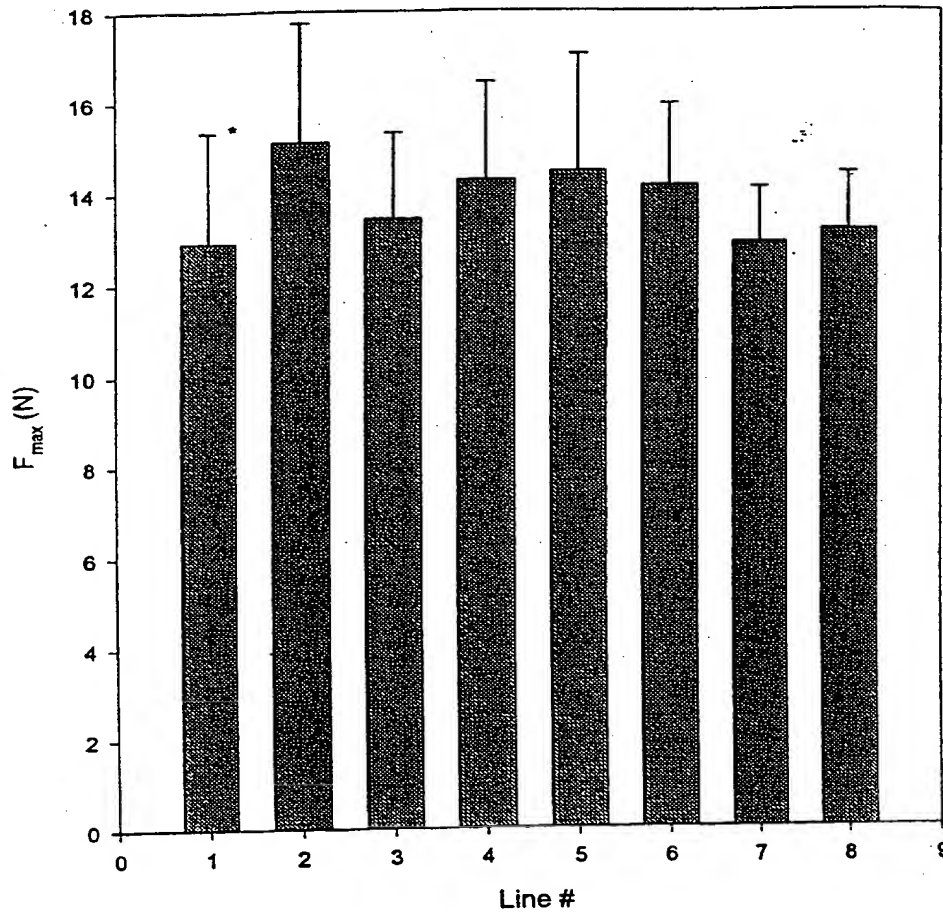


• Standard Deviation

CY07 LINE#	CY07 Mean	CY07 Std Dev
1	8.62	1.69
5	11.07	1.96
6	9.31	1.33
7	10.07	1.81
8	10.18	1.88
9	10.27	1.26
11	9.15	1.30
12	7.99	1.33

Figure 11D

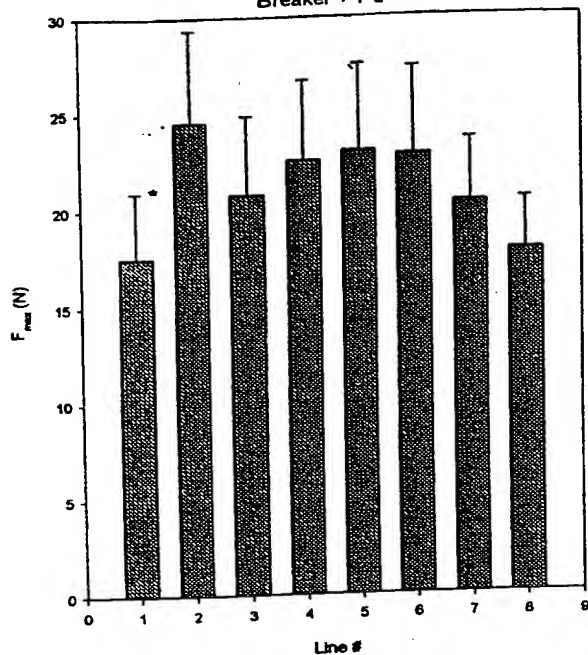
4-mm cylindrical puncture to 1 mm  
Breaker + 7.8



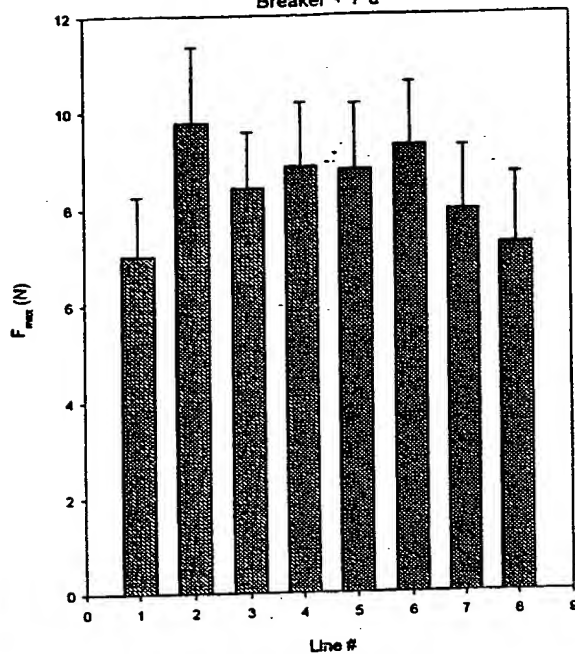
\* Standard Deviation

PU07 Line#	PU07 Mean	PU07 Std Dev
1	12.91	2.43
5	15.13	2.61
6	13.44	1.90
7	14.28	2.16
8	14.47	2.58
9	14.14	1.81
11	12.90	1.20
12	13.18	1.25

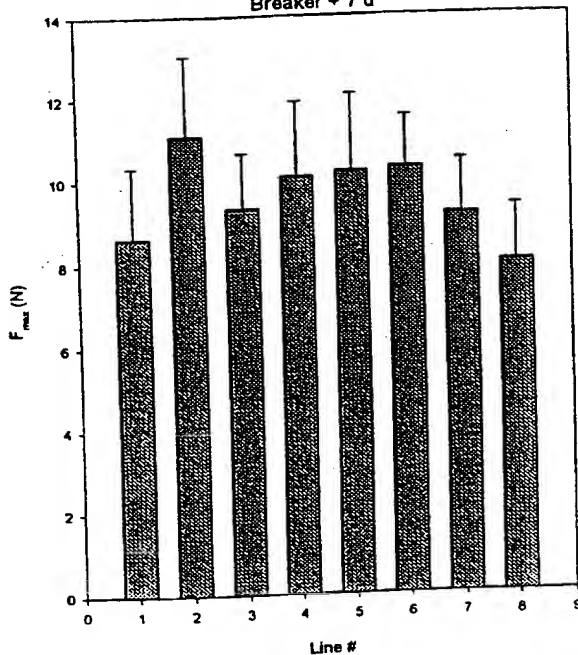
**FIG. 11E(1)**  
Flat plate compression to 3 mm  
Breaker + 7 d



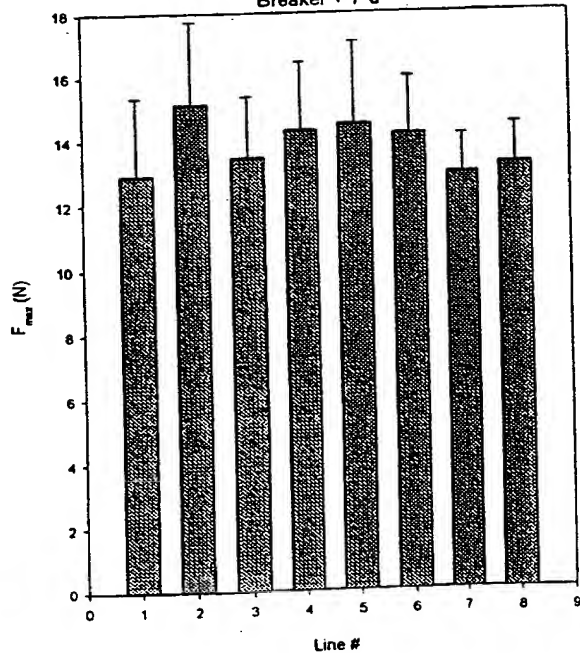
**FIG. 11E(2)**  
Spherical indenter to 3 mm  
Breaker + 7 d



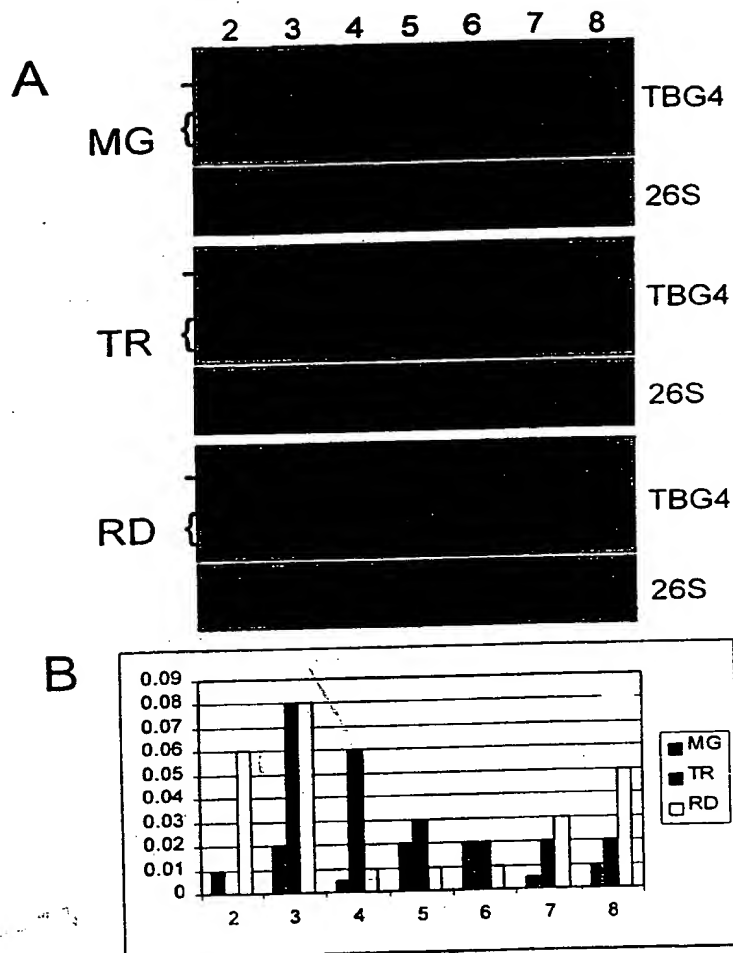
**FIG. 11E(3)**  
4-mm cylindrical indenter to 3 mm  
Breaker + 7 d



**FIG. 11E(4)**  
4-mm cylindrical puncture to 10 mm  
Breaker + 7 d



\* Standard Deviation



**Figure 12. Northern blot analysis of TBG4 expression in transgenic fruit containing TBG4 antisense construct.** A. Total RNA was extracted from mature green/42 days post-pollination (MG), turning/breaker + 3 (TR) and red/breaker + 7 (RD) fruit and twenty  $\mu$ g was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control. The marks - and { denote the positions of the endogenous TBG4 and antisense mRNAs respectively. Lanes 2-8 correspond to transgenic lines 2-8 in Figures 11A-E. B. Chart of TBG4 mRNA levels in lines 2-8. Autoradiographs were scanned using a densitometer and TBG4 mRNA levels were corrected against the loading controls. TBG4 mRNA levels are shown in arbitrary units.

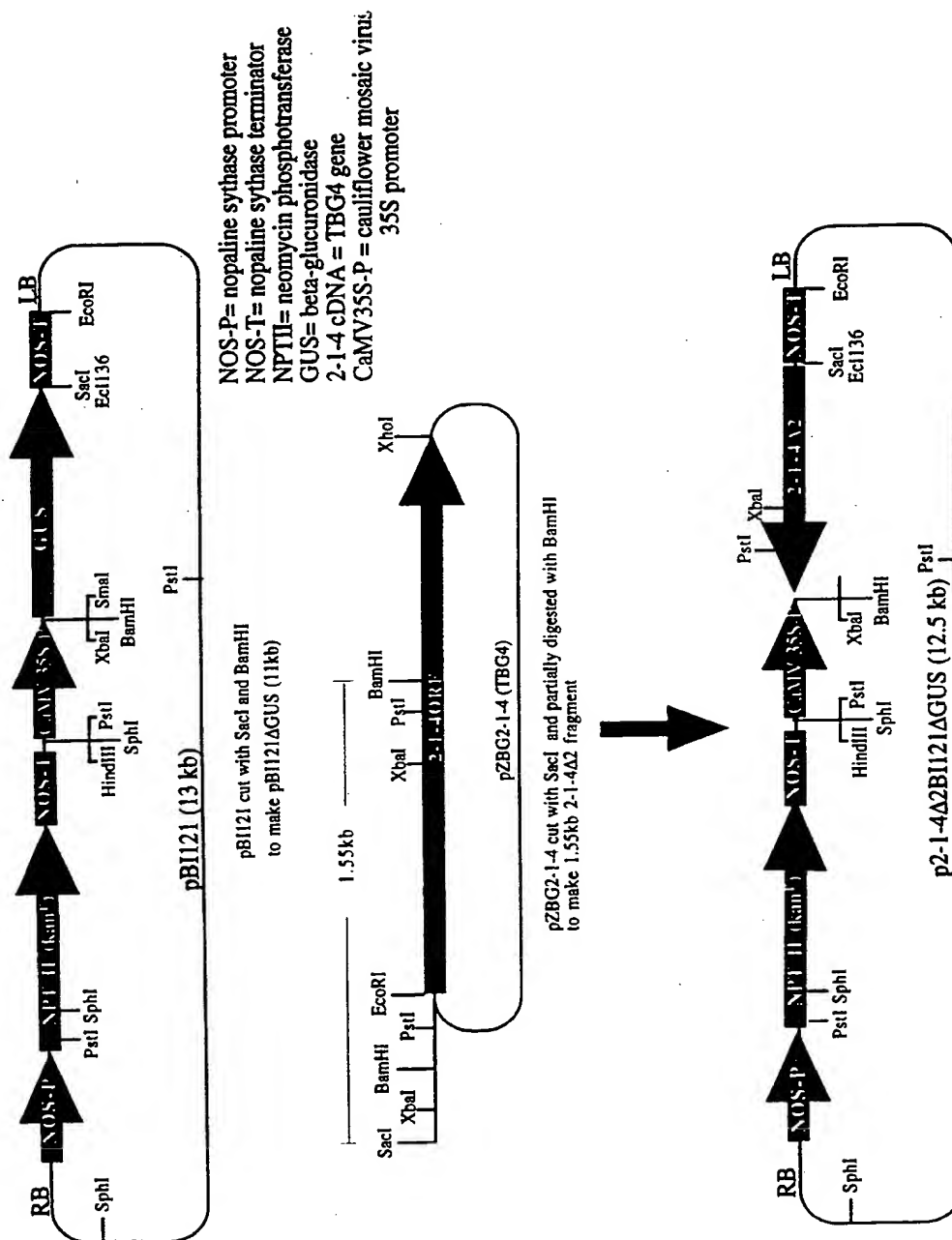


Figure 13. Binary construct used to transform plants and express TBG4 (pZBG2-1-4) in the antisense orientation.